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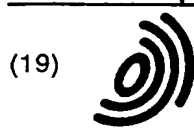
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The applicant has subsequently filed a sequence listing and declared, that it includes no new matter.

(54) **Recombinant thermostable enzyme which releases trehalose from non-reducing saccharide**

(57) Disclosed is a recombinant thermostable enzyme which has a molecular weight of about 54,000-64,000 daltons and a pI of about 5.6-6.6, and releases trehalose from non-reducing saccharides having a trehalose structure as an end unit and a degree of glucose polymerization of at least 3. The enzyme has a sat-

isfactorily-high thermostability, i.e. it is not substantially inactivated even when incubated in an aqueous solution (pH 7.0) at 85°C for 60 min, and this facilitates the production of trehalose on an industrial scale and in a satisfactory-high yield.

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Description

The present invention relates to a recombinant thermostable enzyme which releases trehalose from non-reducing saccharides having a trehalose structure as an end unit and a degree of glucose polymerization of at least 3.

Trehalose is a disaccharide which consists of 2 glucose molecules that are linked together with their reducing groups, and, naturally, it is present in fungi, algae, insects, etc., in an extremely small quantity. Having no reducing residue within the molecule, trehalose does not cause an unsatisfactory browning reaction even when heated in the presence of amino acids or the like, and because of this it can advantageously sweeten food products without fear of causing unsatisfactory coloration and deterioration. Trehalose, however, could not have been readily prepared in a desired amount by conventional production methods, so that it has not scarcely been used for sweetening food products.

Conventional production methods are roughly classified into 2 groups, i.e. the one using cells of microorganisms and the other using a multi-enzymatic system where several enzymes are allowed to act on saccharides. The former, as disclosed in Japanese Patent Laid-Open No.154,485/75, is a method which comprises growing microorganisms such as bacteria and yeasts in nutrient culture media, and collecting trehalose mainly from the proliferated cells. The latter, as disclosed in Japanese Patent Laid-Open No.216,695/83, is a method which comprises providing maltose as a substrate, allowing a multi-enzymatic system using maltose- and trehalose-phosphorylases to act on maltose, and recovering the formed trehalose from the reaction system. The former facilitates the growth of microorganisms, but has a demerit that the content in the microorganisms is at most 15 w/w %, on a dry solid basis (d.s.b.). Although the latter can readily separate trehalose, it is theoretically difficult to increase the trehalose yield by allowing such phosphorylases to act on substrates at a considerably-high concentration because the enzymatic reaction in itself is an equilibrium reaction of 2 different types of enzymes and the equilibrium point constantly inclines to the side of forming glucose phosphate.

In view of the foregoing, the present inventors energetically screened enzymes which form saccharides having a trehalose structure from amylaceous saccharides, and have found that microorganisms such as those of the genera *Rhizobium* and *Arthrobacter* produce an absolutely novel enzyme which forms non-reducing saccharides having a trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of at least 3. They disclosed such an enzyme in Japanese Patent Application No.349,216/93. At almost the same time, they also found that these non-reducing saccharides are nearly quantitatively hydrolyzed into trehalose and glucose and/or maltooligosaccharides by other enzymes produced from the same microorganisms of the genera *Rhizobium* and *Arthrobacter*.

It was found that the enzymes produced from the aforesaid microorganisms have an optimum temperature of about 40°C, and have some difficulties in their thermostability when actually used to produce trehalose. It is recognized in this field that a recommendable temperature in the saccharification reaction of starch or amylaceous saccharides is one which exceeds 55°C because bacterial contamination will occur at a temperature of 55°C or lower and decreasing the pH of the reaction mixtures and inactivating the enzymes used. Thus, a relatively-large amount of substrates remain intact. While the use of enzymes with a poor thermostability, a great care should be taken to control the pH, and, when the pH level lowers to an extremely low level, alkalis should be added to reaction mixtures to increase the pH level as quickly as possible.

In view of the foregoing, the present inventors screened thermostable enzyme with a satisfactory activity and have found that enzymes produced from microorganisms of the genus *Sulfolobus* including *Sulfolobus acidocaldarius* (ATCC 33909) are not substantially inactivated even when incubated at a temperature exceeding 55°C, and they efficiently release trehalose from non-reducing saccharides having a trehalose structure as an end unit and a degree of glucose polymerization of at least 3. These microorganisms, however, are not sufficient in the enzyme productivity, and this requires a relatively-large scale culture to industrially produce trehalose from those non-reducing saccharides.

Recently, the recombinant DNA technology has made a remarkable progress. At present, even an enzyme whose total amino acid sequence has not been revealed can be readily prepared in a desired amount, if once a gene encoding the enzyme is isolated and the base sequence is decoded, by preparing a recombinant DNA containing a DNA that encodes the enzyme, introducing the recombinant DNA into microorganisms or cells of plants or animals, and culturing the resultant transformants. Under these circumstances, urgently required are to find a gene that encodes the thermostable enzyme and to decode the base sequence.

It is an aim of the present invention to provide a recombinant thermostable enzyme which releases trehalose from non-reducing saccharides having a trehalose structure as an end unit and a degree of glucose polymerization of at least 3 by using the recombinant DNA technology.

It is a further aim of the present invention to provide a DNA which encodes the recombinant thermostable enzyme.

It is yet another aim of the present invention to provide a replicable recombinant DNA which contains the DNA.

It is another aim of the present invention to provide a transformant into which the recombinant DNA is introduced.

It is yet another aim of the present invention to provide a process for preparing the recombinant thermostable enzyme using the transformant.

It is another aim of the present invention to provide an enzymatic conversion method for releasing trehalose from

non-reducing saccharides having a trehalose structure as an end unit and a degree of glucose polymerization of at least 3.

The first aim of the present invention is attained by a recombinant thermostable enzyme having the following physicochemical properties:

(1) Action

Releasing trehalose from non-reducing saccharides having a trehalose structure as an end unit and a degree of glucose polymerization of at least 3;

(2) Molecular weight

About 54,000-64,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE);

(3) Isoelectric point (pI)

About 5.6-6.6 on isoelectrophoresis; and

(4) Thermostability

Substantially not inactivated even when incubated in an aqueous solution (pH 7.0) at 85°C for 60 min.

The second aim of the present invention is attained by a DNA which encodes the recombinant thermostable enzyme.

The third aim of the present invention is attained by a replicable recombinant DNA which contains a self-replicable vector and the recombinant thermostable enzyme.

The fourth aim of the present invention is attained by a transformant which is prepared by introducing the replicable recombinant DNA into an appropriate host.

The fifth aim of the present invention is attained by a process for preparing the recombinant thermostable enzyme which comprises culturing the transformant in a nutrient culture medium, and collecting the formed recombinant thermostable enzyme from the culture.

The sixth aim of the present invention is attained by an enzymatic conversion method of non-reducing saccharides having a trehalose structure as an end unit and a degree of glucose polymerization of at least 3, which contains a step of allowing the recombinant thermostable enzyme to act on the non-reducing saccharides to release trehalose.

The invention will now be described, by way of example only, with reference to the accompanying drawings in which:-

FIG.1 is a figure of the optimum temperature of a thermostable enzyme produced from *Sulfolobus acidocaldarius* (ATCC 33909).

FIG.2 is a figure of the optimum pH of a thermostable enzyme produced from *Sulfolobus acidocaldarius* (ATCC 33909).

FIG.3 is a figure of the thermostability of a thermostable enzyme produced from *Sulfolobus acidocaldarius* (ATCC 33909).

FIG.4 is a figure of the pH stability of a thermostable enzyme produced from *Sulfolobus acidocaldarius* (ATCC 33909).

FIG.5 is a restriction map of the recombinant DNA pSU18 according to the present invention.

The recombinant thermostable enzyme according to the present invention releases trehalose from non-reducing saccharides having a trehalose structure as an end unit and a degree of glucose polymerization of at least 3 without substantial inactivation even when allowed to react at a temperature exceeding 55°C.

The DNA according to the present invention expresses the production of the present enzyme by introducing the DNA into an appropriate self-replicable vector to form a replicable recombinant DNA, and introducing the replicable recombinant DNA into an appropriate host which does not produce the present enzyme in itself but readily proliferates.

The recombinant DNA according to the present invention expresses the production of the present enzyme by introducing it into an appropriate host which does not produce the present enzyme but readily proliferates.

The transformant according to the present invention produces the present enzyme when cultured.

Culturing of the transformant by the present process facilitates the production of the present enzyme in a desired amount.

According to the present enzymatic conversion method converts non-reducing saccharides having a trehalose structure as an end unit and a degree of glucose polymerization of at least 3 into saccharide compositions containing trehalose and glucose and/or maltooligosaccharides.

The present invention has been made based on the finding of a novel enzyme which releases trehalose from non-reducing saccharides having a trehalose structure as an end unit and a degree of glucose polymerization of at least 3. Such an enzyme is obtainable from cultures of microorganisms of the species *Sulfolobus acidocaldarius* (ATCC 33909). The present inventors isolated such an enzyme by using in combination a various purification methods comprising column chromatography as a main technique, studied their properties and features, and revealed that the reality is a

polypeptide with the following physicochemical properties:

(1) Action

Releasing trehalose from non-reducing saccharides having a trehalose structure as an end unit and a degree of glucose polymerization of at least 3;

(2) Molecular weight

About 54,000-64,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE);

(3) Isoelectric point (pI)

About 5.6-6.6 on isoelectrophoresis; and

(4) Optimum temperature

Exhibiting an optimum temperature of about 75°C when incubated at a pH 6.0 for 30 min;

(5) Optimum pH

Exhibiting an optimum pH of about 5.5-6.0 when incubated at 60°C for 30 min;

(6) Thermostability

Stable up to a temperature of about 85°C even when incubated at a pH 7.0 for 60 min; and

(7) pH Stability

Stable up to a pH of about 5.5-9.5 when incubated at 25°C for 16 hours.

The followings are the explanations of the experiments conducted to reveal the physicochemical properties of a thermostable enzyme produced from *Sulfolobus acidocaldarius* (ATCC 33909):

Experiment 1

Preparation of purified enzyme

Into 500-ml flasks were poured 100 ml aliquots of a liquid culture medium containing 0.1 w/v % polypeptone, 0.1 w/v % yeast extract, 0.2 w/v % ammonium sulfate, 0.05 w/v % potassium dihydrogen phosphate, 0.02 w/v % magnesium sulfate heptahydrate, 0.02 w/v % potassium chloride, and water, and the flasks were sterilized by autoclaving at 120°C for 20 min. After cooling the flasks a seed culture of *Sulfolobus acidocaldarius* (ATCC 33909) was inoculated into each liquid culture medium in each flask, followed by the incubation at 75°C for 24 hours under a rotary shaking condition of 130 rpm to obtain a first seed culture. About 5 L of a fresh preparation of the same liquid culture medium was poured into a 10-L fermenter, sterilized similarly as above, cooled to 75°C, and adjusted to a pH 3.0, followed by inoculating one v/v % of the first seed culture into the sterilized liquid culture medium in the fermenter, and culturing the microorganisms at 75°C for 24 hours under an aeration condition of 500 ml/min. Thereafter, about 250 L of a fresh preparation of the same liquid culture medium was poured into a 300-L fermenter, sterilized similarly as above, cooled to 75°C, and adjusted to a pH 3.0, followed by inoculating one v/v % of the second seed culture into the sterilized liquid culture medium, and culturing the microorganisms at 75°C for 42 hours under an aeration condition of 100 L/min.

About 170 L of the resultant culture was filtered with an SF membrane, and the filtrate was centrifuged to obtain wet cells. About 258 g of the wet cells was suspended in 300 ml of 10 mM phosphate buffer (pH 7.0) and ultrasonicated to disrupt them. The cell debris thus obtained was centrifuged at 10,000 rpm for 30 min, and about 300 ml of the resultant supernatant was mixed with ammonium sulfate to give a saturation degree of 70 w/v %, allowed to stand at 4°C for 24 hours, and centrifuged at 10,000 rpm for 30 min. The precipitate was collected, dissolved in an adequate amount of 10 mM Tris-HCl buffer (pH 8.5), and dialyzed against a fresh preparation of the same buffer for 24 hours. Thereafter, the dialyzed solution was centrifuged at 10,000 rpm for 30 min to obtain an about 300 ml of a supernatant with an enzymatic activity.

The supernatant was fed to a column packed with about 360 ml of "DEAE-TOYOPEARL®", a gel for ion-exchange column chromatography commercialized by Tosoh Corporation, Tokyo, Japan, and fed with a linear gradient buffer ranging from 0 M to 0.3 M in 10 mM Tris-HCl buffer (pH 8.5). Fractions with an enzymatic activity, eluted at a concentration of about 0.1 M sodium chloride, were collected, pooled, and dialyzed for 10 hours against 10 mM Tris-HCl buffer (pH 8.5) containing one M ammonium sulfate. The dialyzed solution was centrifuged to remove insoluble substances, fed to a column packed with about 350 ml of "BUTYL-TOYOPEARL® 650", a gel for hydrophobic chromatography commercialized by Tosoh Corporation, Tokyo, Japan, which had been previously equilibrated with 10 mM Tris-HCl buffer (pH 8.5)

containing one M ammonium sulfate, and fed with a linear gradient buffer ranging from 1 M to 0 M ammonium sulfate in 10 mM Tris-HCl buffer (pH 8.5).

Fractions with an enzymatic activity eluted at about 0.2 M ammonium sulfate were collected, pooled, dialyzed for 16 hours against 10 mM Tris-HCl buffer (pH 8.5) containing 0.2 M sodium chloride, and centrifuged to remove insoluble substances. The resultant supernatant was fed to a column packed with about 350 ml of "TOYOPEARL® HW-55", a gel for gel chromatography commercialized by Sepracor, Massachusetts, USA, which had been previously equilibrated with 10 mM Tris-HCl buffer (pH 8.5) containing 0.2 M sodium chloride. Fractions with an enzymatic activity were collected from the eluate, pooled, and dialyzed against 10 mM Tris-HCl buffer (pH 8.5) for 16 hours. The dialyzed solution was centrifuged to remove insoluble substances, and the supernatant was fed to a column packed with about 10 ml of "SUPERROSE 12 HR 10/30", a product of Pharmacia LKB Uppsala, Sweden, which had been previously equilibrated with 10 mM Tris-HCl buffer (pH 8.5), and eluted with 10 mM Tris-HCl buffer (pH 8.5). Fractions with an enzymatic activity eluted at about 0.1 M sodium chloride were collected and pooled for use in the following experiments. The purified enzyme thus obtained had a specific activity of about 378 units/mg protein, and the yield was about 0.86 units per one L of the culture.

The purified protein was in usual manner electrophoresed in 7.5 w/v % polyacrylamide gel to find a substantially single protein band with an enzymatic activity. This indicated that the purified protein was extremely pure.

Throughout the specification the activity of the present thermostable enzyme is expressed by the value measured on the following assay: Place 4 ml of 50 mM phosphate buffer (pH 6.0) containing as a substrate 1.25 w/v % α -maltotriosyltrehalose in a test tube, add one ml of an adequately diluted enzyme solution to the test tube, and incubate the mixture solution at 60°C for 30 min to effect enzymatic reaction. Thereafter, one ml of the reaction mixture is mixed with 2 ml of the Somogyi copper solution to suspend the enzymatic reaction, followed by assaying the reducing power on the Somogyi-Nelson's method. As a control, a system using an enzyme solution, which has been heated at 100°C for 30 min to inactivate the enzyme, is provided and similarly treated as above. One unit activity of the thermostable enzyme is defined as the amount of enzyme which increases the reducing power of one μ mol glucose per min under the same conditions as mentioned above.

Experiment 2

Physicochemical property of thermostable enzyme

Experiment 2-1

Action

α -Glucosyltrehalose, α -maltosyltrehalose, α -maltotriosyltrehalose, α -maltotetraosyltrehalose or α -maltopentaosyltrehalose as a substrate was dissolved in 50 mM acetate buffer (pH 5.5) into a 20 w/v % solution which was then admixed with 2 units/g substrate, d.s.b., of the purified thermostable enzyme in Experiment 1, and subjected to an enzymatic reaction at 60°C for 48 hours. The reaction mixture was desalted in usual manner, and the saccharide composition of the resultant solution was analyzed on high-performance liquid chromatography (HPLC) using a column of "WAKOBEADS WB-T-330", a column for HPLC commercialized by Wako Pure Chemical Industries, Ltd., Tokyo, Japan. The HPLC procedure was carried out at ambient temperature, and water was used as an eluant and fed to the column at a flow rate of 0.5 ml/min while monitoring the eluate on "MODEL RI-8012", a differential refractometer commercialized by Tosoh Corporation, Tokyo, Japan. As a control, 5 systems using as a substrate maltotriose, maltotetraose, maltopentaose, maltohexaose and maltoheptaose were respectively provided, and similarly treated as above. The results were in Table 1.

Table 1

Substrate	Saccharide in reaction mixture	Elution time on HPLC (min)	Composition (%)
α -Glucosyltrehalose	Trehalose	27.4	7.2
	Glucose	33.8	3.9
	α -Glucosyltrehalose	23.3	88.9
α -Maltosyltrehalose	Trehalose	27.4	40.2
	Maltose	28.7	40.5
	α -Maltosyltrehalose	21.6	19.3
α -Maltotriosyltrehalose	Trehalose	27.4	41.1
	Maltotriose	25.9	58.2
	α -Maltotriosyltrehalose	19.7	0.7
α -Maltotetraosyltrehalose	Trehalose	27.4	34.0
	Maltotetraose	24.1	65.8
	α -Maltotetraosyltrehalose	18.7	0.2
α -Maltopentaosyltrehalose	Trehalose	27.4	29.1
	Maltopentaose	22.6	70.6
	α -Maltopentaosyltrehalose	17.8	0.3
Maltotriose	Maltotriose	25.9	100
Maltotetraose	Maltotetraose	24.1	100
Maltopentaose	Maltopentaose	22.6	100
Maltohexaose	Maltohexaose	21.8	100
Maltoheptaose	Maltoheptaose	21.0	100

The results in Table 1 show that the purified enzyme nearly quantitatively releases trehalose and glucose or mal-

tooligosaccharides from non-reducing saccharides having a trehalose structure as an end unit and a degree of glucose polymerization of at least 3, but does not substantially act on maltooligosaccharides having a degree of glucose polymerization of at least 3. These facts indicate that the purified enzyme specifically acts on non-reducing saccharides having a trehalose structure as an end unit and a degree of glucose polymerization of at least 3, and specifically hydrolyzes the glycosidic linkages between trehalose- and glycosyl-residues. Such an enzyme has not been reported and it can be estimated to have a novel enzymatic pathway.

Experiment 2-2

Molecular weight

In accordance with the method reported by U. K. Laemmli in *Nature*, Vol.227, pp.680-685 (1970), the purified enzyme in Experiment 1 was electrophoresed on SDS-PAGE to give a single protein band with an enzymatic activity at a position corresponding to about 54,000-64,000 daltons. The marker proteins used in this experiment were myosin (MW=200,000 daltons), β -galactosidase (MW=116,250 daltons), phosphorylase B (MW=97,400 daltons), serum albumin (MW=66,200 daltons) and ovalbumin (MW=45,000 daltons).

Experiment 2-3

Isoelectric point

The purified enzyme in Experiment 1 gave an isoelectric point of about 5.6-6.6 when isoelectrophoresed in a polyacrylamide gel containing 2 w/v % ampholine.

Experiment 2-4

Optimum temperature

As is shown in FIG.1, the optimum temperature of the purified enzyme in Experiment 1 was about 75°C when incubated in usual manner in 20 mM phosphate buffer (pH 6.0) at different temperatures for 30 min.

Experiment 2-5

Optimum pH

As is shown in FIG.2, the optimum pH of the purified enzyme in Experiment 1 was about 5.5-6.0 when incubated in usual manner at 60°C for 30 min in McIlvaine buffer with different pHs.

Experiment 2-6

Thermal stability

As is shown in FIG.3, the purified enzyme in Experiment 1 was stable up to a temperature of about 85°C when incubated in usual manner in 50 mM phosphate buffer (pH 7.0) for 60 min.

Experiment 2-7

pH Stability

As is shown in FIG.4, the purified enzyme in Experiment 1 was stable at a pH in the range of about 5.5-9.5 when incubated in usual manner at 25°C for 16 hours in McIlvaine buffer or 50 mM sodium carbonate/sodium hydrogen carbonate buffer with different pHs.

Experiment 2-8

Amino acid sequence containing the N-terminal

The amino acid sequence containing the N-terminal of the purified enzyme in Experiment 1 was analyzed on "MOD-

EL 473 A*, a gas-phase protein sequencer commercialized by Perkin-Elmer Corp., Instrument Div., Norwalk, USA, and revealing that it has the amino acid sequence in SEQ ID NO:3.

Experiment 2-9

Partial amino acid sequence

An adequate amount of the purified enzyme in Experiment 1 was weighed, dialyzed against 10 mM Tris-HCl buffer (pH 9.0) at 4°C for 18 hours, and admixed with 10 mM Tris-HCl buffer (pH 9.0) to give a concentration of about one mg/ml of the enzyme. About one ml of the resultant solution was placed in a container, admixed with 10 µg lysyl endopeptidase, and incubated at 30°C for 64 hours to partially hydrolyze the enzyme. The resultant hydrolysate was applied to "µBONDAPAK C18", a column for HPLC commercialized by Japan Millipore Ltd., Tokyo, Japan, which had been previously equilibrated with 0.1 v/v % trifluoroacetate containing 8 v/v % aqueous acetonitrile, followed by feeding to the column 0.1 v/v % trifluoroacetate at a flow rate of 0.9 ml/min while increasing the concentration of aqueous acetonitrile from 8 to 48 v/v %, and collecting fractions containing a peptide fragment eluted about 57 min after the initiation of the feeding. The fractions were pooled, dried *in vacuo*, and dissolved in 0.1 v/v % trifluoroacetate containing 50 v/v % aqueous acetonitrile. Similarly as in Experiment 2-8, the peptide fragment was analyzed and revealed to have an amino acid sequence in SEQ ID NO:4.

Such an enzyme having these physicochemical properties has not been known and meaning that it is a novel enzyme.

A chromosomal DNA of *Sulfolobus acidocaldarius* (ATCC 33909) was screened by using an oligonucleotide as a probe which had been chemically synthesized based on the partial amino acid sequences in SEQ ID NOs:3 and 4, and this yielded a DNA fragment having a base sequence from the 5'-terminus consisting of about 1,700 base pairs in SEQ ID NO:2. The base sequence of the thermostable enzyme was decoded and revealing that it consists of 556 amino acids and has a partial amino acid sequence from the N-terminal in SEQ ID NO:1.

The sequential experimental steps used to reveal the amino acid sequence and the base sequence in SEQ ID NOs:1 to 2 are summarized in the below:

(1) A thermostable enzyme was isolated from a culture of a donor microorganism, highly purified, and determined for the N-terminal amino acid sequence. The purified enzyme was partially hydrolyzed with protease, and from which a peptide fragment was isolated and determined for amino acid sequence;

(2) A chromosomal DNA was isolated from a donor microorganism, purified and partially digested with a restriction enzyme to obtain a DNA fragment consisting of about 2,000-6,000 base pairs. The DNA fragment was ligated by DNA ligase to a plasmid vector, which had been previously cleaved with a restriction enzyme, to obtain a recombinant DNA;

(3) The recombinant DNA thus obtained was introduced into *Escherichia coli* to obtain transformants, and from which an objective transformant containing a DNA which encodes the objective enzyme was selected by the colony hybridization method using as a probe an oligonucleotide which had been chemically synthesized based on the above partial amino acid sequence; and

(4) The recombinant DNA was obtained from the transformant and annealed with a primer, followed by allowing a DNA polymerase to act on the resultant to extend the primer, and determining the base sequence of the resultant complementary chain DNA by the dideoxy chain termination method. The comparison of an amino acid sequence, that could be estimated from the base sequence, with the aforesaid amino acid sequence confirmed that the base sequence encodes the enzyme.

The following Experiments 3 and 4 will concretely explain the above steps (2) to (4), and the techniques in themselves used therein are well known in this art, for example, those described by J. Sambrook et al. in "Molecular Cloning A Laboratory Manual", 2nd edition, published by Cold Spring Harbor Laboratory Press, USA (1989).

Experiment 3Preparation of recombinant DNA containing DNA which encodes thermostable enzyme, and transformant obtained therewithExperiment 3-1Preparation of chromosomal DNA

To 500-ml flasks were placed about 100 ml aliquots of a liquid culture medium consisting of 0.1 w/v % polypeptone, 0.1 w/v % yeast extract, 0.2 w/v % ammonium sulfate, 0.05 w/v % potassium dihydrogen phosphate, 0.02 w/v % magnesium sulfate heptahydrate, 0.02 w/v % potassium chloride, and water, and the flasks were sterilized by autoclaving at 120°C for 20 min, cooled, and adjusted to a pH 3.0 by the addition of sulfate. A seed culture of *Sulfolobus acidocaldarius* (ATCC 33909) was inoculated into each flask, incubated at 75°C for 24 hours under a rotary shaking condition of 130 rpm to obtain a seed culture. About 5 L of a fresh preparation of the same liquid nutrient culture medium was placed in a 10-L fermenter, sterilized similarly as above, cooled to 75°C, adjusted to a pH 3.0, and inoculated with one v/v % of the seed culture, followed by the incubation at 75°C for 24 hours under an aeration condition of 500 ml/min.

The resultant cells were collected by centrifugation, suspended in TES buffer (pH 8.0), admixed with 0.05 w/v % lysozyme, and incubated at 37°C for 30 min. The resultant was frozen at -80°C for one hour, admixed with TSS buffer (pH 9.0), heated to 60°C, and admixed with a mixture solution of TES buffer and phenol, and the resultant mixture was chilled with ice and centrifuged to obtain a supernatant. To the supernatant was added 2 fold volumes of cold ethanol to precipitate a crude chromosomal DNA which was then collected, dissolved in SSC buffer (pH 7.1), admixed with 7.5 µg ribonuclease and 125 µg protease, and incubated at 37°C for one hour. Thereafter, a mixture solution of chloroform and isoamyl alcohol was added to the reaction mixture to extract the objective chromosomal DNA. The resultant extract was admixed with cold ethanol, followed by collecting the formed sediment containing a chromosomal DNA. The chromosomal DNA thus purified was dissolved in SSC buffer (pH 7.1) to give a concentration of about one mg/ml, and the solution was frozen at -80°C.

Experiment 3-2Preparation of recombinant DNA pSU18 and transformant SU18

One ml of the purified chromosomal DNA in Experiment 3-1 was placed in a container, admixed with about 35 units of *Sau* 3AI, a restriction enzyme, and enzymatically reacted at 37°C for 20 min to partially digest the chromosomal DNA, followed by recovering a DNA fragment consisting of about 2,000-6,000 base pairs by sucrose density-gradient ultracentrifugation. One µg of Bluescript II SK(+), a plasmid vector commercialized by Stratagene Cloning Systems, California, USA, was weighed, subjected to the action of *Bam* HI, a restriction enzyme, to completely digest the plasmid vector, and admixed with 10 µg of the DNA fragment and 2 units of T4 DNA ligase. The mixture was allowed to stand at 4°C overnight to ligate the DNA fragment to the plasmid vector. To the resultant recombinant DNA was added 30 µl of "Epicurian Coli® XLI-Blue", a competent cell commercialized by Toyobo Co., Ltd., Tokyo, Japan, allowed to stand under ice-chilling conditions for 30 min, heated to 42°C, admixed with SOC broth, and incubated at 37°C for one hour to introduce the recombinant DNA into *Escherichia coli*.

The transformant thus obtained was inoculated into agar plate (pH 7.0) containing 50 µg/ml of 5-bromo-4-chloro-3-indolyl-β-galactoside, and cultured at 37°C for 18 hours, followed by placing a nylon film on the agar plate to fix thereon about 7,000 colonies formed on the agar plate. Based on the amino acid sequence of Phe-Lys-Leu-Trp-Ala-Pro of the amino acid sequence in SEQ ID NO:3, probe 1 represented by the base sequence of 5'-TTYAARYTNTGGGC-NCC-3' was chemically synthesized, labelled with ³²P, and hybridized with the colonies of transformants fixed on the nylon film, followed by selecting 12 transformants which exhibited a strong hybridization.

The objective recombinant DNA was selected in usual manner from the 12 transformants, and, in accordance with the method described by E. M. Southern in *Journal of Molecular Biology*, Vol.98, pp.503-517 (1975), hybridized with probe 2 having the base sequence of 5'-CARTGGGTNGAYGAYTTYCA-3' which had been chemically synthesized based on the amino acid sequence of Gln-Trp-Val-Asp-Asp-Phe-His in SEQ ID NO:4 and labelled with ³²P, followed by selecting a recombinant DNA which exhibited a strong hybridization. The recombinant DNA and transformant were respectively named "pSU18" and "SU18".

The transformant SU18 was inoculated into L-broth (pH 7.0) containing 100 µg/ml ampicillin, and cultured at 37°C for 24 hours with a rotary shaker. After completion of the culture, the cells were collected from the culture by centrifugation, and treated with the alkaline method in general to extracellularly extract the recombinant DNA. The resultant extract was in usual manner purified and analyzed to find that the recombinant DNA pSU18 consists of about 6,000 base pairs

and has a DNA, which encodes the enzyme and consists of about 1,700 base pairs, in the downstream of the cleavage site of *Ssp I*, a restriction enzyme.

Experiment 3-3

Production of recombinant thermostable enzyme by transformant SU18

To 500-ml flasks were added about 100 ml aliquots of a liquid culture medium (pH 7.0) consisting of 0.1 w/v % polypeptone, 0.1 w/v % yeast extract, 0.2 w/v ammonium sulfate, 0.05 w/v % potassium dihydrogen phosphate, 0.02 w/v % magnesium sulfate heptahydrate, 0.02 w/v % potassium chloride, and water. The flasks were sterilized by autoclaving at 120°C for 20 min, cooled, admixed with 50 µg/ml ampicillin, and inoculated with a seed culture of transformant SU18 in Experiment 3-2, followed by culturing the transformant at 37°C for 24 hours under a rotary shaking condition of 130 rpm to obtain a seed culture. About 5 L of a fresh preparation of the same liquid culture medium was placed in a 10-L fermenter, sterilized similarly as above, cooled to 37°C, admixed with 50 µg/ml ampicillin, inoculated with one v/v % of the seed culture, followed by the incubation at 37°C for 24 hours under an aeration condition of 500 ml/min. The resultant culture was in usual manner treated with ultrasonic to disrupt cells, and the resultant suspension was centrifuged to remove insoluble substances, followed by assaying for enzymatic activity to reveal that one L of the culture contained about 30 units of the recombinant thermostable enzyme.

As a control, a seed culture of *Escherichia coli* XLI-Blue strain or *Sulfolobus acidocaldarius* (ATCC 33909) was inoculated into a fresh preparation of the same liquid culture medium but free of ampicillin. In the case of culturing *Sulfolobus acidocaldarius* (ATCC 33909), it was cultured and treated similarly as above except that the initial pH of the nutrient culture medium and the culturing temperature were respectively set to 3.0 and 75°C. Assaying the resultant enzymatic activity, one L culture of *Sulfolobus acidocaldarius* (ATCC 33909) yielded about 2 units of the thermostable enzyme, and the yield was significantly lower than that of transformant SU18. *Escherichia coli* XLI-Blue strain used as a host did not form the thermostable enzyme.

Thereafter, the recombinant thermostable enzyme produced by the transformant SU18 was purified similarly as in Experiments 1 and 2 and examined for properties and features and revealing that it has substantially the same physicochemical properties of the thermostable enzyme from *Sulfolobus acidocaldarius* (ATCC 33909) because (i) the recombinant thermostable enzyme has a molecular weight of about 54,000-64,000 daltons on SDS-PAGE and an isoelectric point of about 5.6-6.6 on isoelectrophoresis, and (ii) it is not substantially inactivated even when incubated in an aqueous solution (pH 7.0) at 85°C for 60 min. These results indicate that the present thermostable enzyme can be prepared by the recombinant DNA technology with a significantly improved yield.

Experiment 4

Preparation of complementary DNA, and determination of base sequence and amino acid sequence

Two µg of the recombinant DNA pSU18 in Experiment 3-2 was weighed, degenerated by the addition of 2 M aqueous sodium hydroxide solution, and admixed with an adequate amount of cold ethanol, followed by collecting the resultant sediment containing a template DNA and drying the sediment *in vacuo*. To the template DNA were added 50 pmole/ml of a chemically synthesized primer having the base sequence of 5'-GTAAAACGACGGCCAGT-3' and 10 µl of 40 mM Tris-HCl buffer (pH 7.5) containing 20 mM magnesium chloride and sodium chloride, and the mixture was incubated at 65°C for 2 min to effect annealing. The resultant mixture was admixed with 2 µl of an aqueous solution containing 7.5 µM dATP, dGTP and dTTP respectively, 0.5 µl of [α -³²P]dCTP (2 mCi/ml), one µl of 0.1 M dithiothreitol, and 2 µl of 1.5 units/ml T7 DNA polymerase, followed by the incubation at 25°C for 5 min to extend the primer from the 5'-terminus to the 3'-terminus. Thus, a complementary chain DNA was obtained.

The reaction product containing the complementary chain DNA was divided into quarters, to each of which 2.5 µl of 50 mM aqueous sodium chloride solution containing 80 µM dNTP and 8 µM ddATP, ddCTP, ddGTP or ddTTP was added, and the resultant mixture was incubated at 37°C for 5 min, followed by suspending the reaction by the addition of 4 µl of 98 v/v % aqueous formamide solution containing 20 mM EDTA, 0.05 w/v % bromophenol blue and 0.05 w/v % xylene cyanol. The reaction mixture was placed in a container, heated in a boiling-water bath for 3 min, placed on a gel containing 6 w/v % polyacrylamide, and electrophoresed by energizing the gel with a constant voltage of about 2,000 volts to separate DNA fragments, followed by fixing the gel in usual manner, drying it and subjecting the resultant to autoradiography.

Analyses of the DNA fragments separated on the radiogram revealed that the complementary chain DNA contains the base sequence consisting of 1,700 base pairs in SEQ ID NO:5. An amino acid sequence that could be estimated from the base sequence was in SEQ ID NO:5, and it was compared with the partial amino acid sequences in SEQ ID NOs:3 and 4, and revealing that the partial amino acid sequence in SEQ ID NO:3 corresponded to that positioning from

1 to 30 in SEQ ID NO:5, and that in SEQ ID NO:4 corresponded to that positioning from 301 to 319 in SEQ ID NO:5. These results indicate that the present recombinant thermostable enzyme has the amino acid sequence from the N-terminal in SEQ ID NO:1, and, in the case of the DNA derived from *Sulfolobus acidocaldarius* (ATCC 33909), the amino acid sequence is encoded by the base sequence from the 5'-terminus in SEQ ID NO:2.

As is explained in the above, the thermostable enzyme, which releases trehalose from non-reducing saccharides having a trehalose structure as an end unit and a degree of glucose polymerization of at least 3, was found as a result of the present inventors' long-term research. The thermostable enzyme has distinct physicochemical properties from those of other conventional enzymes. The present invention is to produce the thermostable enzyme by using the recombinant DNA technology. The present recombinant thermostable enzyme, its preparation and uses will be explained in detail with reference to the later described Examples.

The recombinant thermostable enzyme as referred to in the present invention means thermostable enzymes in general which are preparable by the recombinant DNA technology and capable of releasing trehalose from non-reducing saccharides having a trehalose structure as an end unit and a degree of glucose polymerization of at least 3. Generally, the recombinant thermostable enzyme according to the present invention has a revealed amino acid sequence, and, as an example, the amino acid sequence from the N-terminal as shown in SEQ ID NO:1, and homologous ones to it can be mentioned. Variants having amino acid sequences homologous to the one in SEQ ID NO:1 can be obtained by replacing one or more bases in SEQ ID NO:1 with other bases without substantially alternating the inherent physicochemical properties. Although even when used the same DNA and it also depends on hosts into which the DNA is introduced, the ingredients and components of nutrient culture media for culturing transformants, and their cultivation temperature and pH, there may be produced modified enzymes which have the inherent physicochemical properties but defect one or more amino acids in SEQ ID NO:1, or those which have one or more amino acids added newly to the N-terminal after the DNA expression as the result of the modification of intracellular enzymes of the hosts. Such variants can be used in the present invention as long as they have the desired physicochemical properties.

The recombinant thermostable enzyme can be obtained from cultures of transformants containing a specific DNA. Examples of such transformants usable in the present invention can be prepared by introducing into hosts a DNA which has either the base sequence from the 5'-terminus in SEQ ID NO:2 or a homologous base sequence to it or a complementary base sequence to them. These base sequences may be modified by replacing one or more bases of them without alternating the amino acid sequences encoded by them by means of the degeneracy of genetic code. Needless to say, one or more bases in such base sequences which encode the recombinant thermostable enzyme or their variants can be readily replaced with other bases to allow the DNA to express the objective thermostable enzyme production in hosts.

The DNA usable in the present invention includes those are derived from natural resources and those which are artificially synthesized as long as they have the aforesaid base sequences. The natural resources for the DNA according to the present invention are, for example, microorganisms of the genus *Sulfolobus* such as *Sulfolobus acidocaldarius* (ATCC 33909), and from which genes containing the present DNA can be obtained. The aforementioned microorganisms can be inoculated in nutrient culture media and cultured for about 1-3 days under aerobic conditions, and the resultant cells were collected from the cultures and subjected to ultrasonication or treated with a cell-wall lysis enzyme such as lysozyme or β -glucanase to extract genes containing the present DNA. In this case, a proteolytic enzyme such as protease can be used along with the cell-wall lysis enzyme, and, when treated the cells with an ultrasonic disintegrator, they may be treated in the presence of a surfactant such as sodium dodecyl sulfate (SDS) or with freezing and thawing method. The objective DNA is obtainable by treating the resultant with phenol extraction, alcohol sedimentation, centrifugation, protease treatment and/or ribonuclease treatment generally used in this field. To artificially synthesize the present DNA, it can be chemically synthesized by using the base sequence in SEQ ID NO:2, or can be obtained in a plasmid form by inserting a DNA, which encodes the amino acid sequence in SEQ ID NO:1, into an appropriate self-replicable vector to obtain a recombinant DNA, introducing the recombinant DNA into an appropriate host to obtain a transformant, culturing the transformant, separating the proliferated cells from the resultant culture, and collecting plasmids containing the objective DNA from the cells.

Such a DNA is generally introduced into hosts in a recombinant DNA form. Generally, the recombinant DNA contains the aforesaid DNA and a self-replicable vector, and it can be prepared with a relative easiness by the recombinant DNA technology in general when the material DNA is in hand. Examples of such a vector are plasmid vectors such as pBR322, pUC18, Bluescript II SK(+), pUB110, pTZ4, pC194, pHV14, TRp7, TEp7, pBS7, etc.; and phage vectors such as λ gt- λ C, λ gt- λ B, p11, ϕ 1, ϕ 105, etc. Among these plasmid- and phage-vectors, pBR322, pUC18, Bluescript II SK(+), λ gt- λ C and λ gt- λ B are satisfactorily used when the present DNA should be expressed in *Escherichia coli*, while pUB110, pTZ4, pC194, p11, ϕ 1 and ϕ 105 are satisfactorily used to express the DNA in microorganisms of the genus *Bacillus*. The plasmid vectors pHV14, TRp7, TEp7 and pBS7 are advantageously used when the recombinant DNA is allowed to grow in 2 or more hosts.

The methods used to insert the present DNA into such vectors in the present invention may be conventional ones in generally used in this field. A gene containing the present DNA and a self-replicable vector are first digested with a

restriction enzyme and/or ultrasonic, then the resultant DNA fragments and vector fragments are ligated. To digest DNAs and vectors, restriction enzymes which specifically act on nucleotides, particularly, type II restriction enzymes, more particularly *Sau* 3A1, *Eco* RI, *Hind* III, *Bam* HI, *Sal* I, *Xba* I, *Sac* I, *Pst* I, etc., facilitate the ligation of the DNA fragments and vector fragments. To ligate the DNA fragments with the vector fragments, they are, if necessary, annealed and subjected to the action of a DNA ligase *in vivo* or *in vitro*. The recombinant DNA thus obtained is replicable without substantial limitation by introducing it into appropriate hosts to form transformants and culturing the transformants.

The recombinant DNA thus obtained can be introduced into appropriate host microorganisms including *Escherichia coli* and those of the genus *Bacillus* as well as actinomyces and yeasts. In the case of using *Escherichia coli* as a host, the DNA can be introduced therein by culturing the host in the presence of the recombinant DNA and calcium ion, while in the case of using a microorganism of the genus *Bacillus* as a host the competent cell method and the colony hybridization method can be used. Desired transformants can be cloned by the colony hybridization method or by culturing a variety of transformants in nutrient culture media containing reducing amylaceous saccharides having a degree of glucose polymerization of at least 3, and selecting the objective transformants which release trehalose from non-reducing saccharides having a trehalose structure as an end unit and a degree of glucose polymerization of at least 3.

The transformants thus obtained intra- and extra-cellularly produce the objective enzyme when cultured in nutrient culture media. Generally, liquid culture media in general supplemented with carbon sources, nitrogen sources and minerals, and, if necessary, further supplemented with small amounts of amino acids and vitamins can be used in the invention. Examples of the carbon sources are saccharides such as unprocessed starch, starch hydrolysate, glucose, fructose, sucrose and trehalose. Examples of the nitrogen sources are organic- and inorganic-substances containing nitrogen such as ammonia and salts thereof, urea, nitrate, peptone, yeast extract, defatted soy bean, corn steep liquor, and beef extract. Cultures containing the objective enzyme can be prepared by inoculating the transformants into nutrient culture media, and incubating them at a temperature of 20-65°C and a pH of 2-9 for about 1-6 days under aerobic conditions by the aeration-agitation method. Such cultures can be used intact as a crude enzyme, and, usually, cells in the cultures may be disrupted prior to use with ultrasonic and/or cell-wall lysis enzymes, followed by separating the thermostable enzyme from intact cells and cell debris by filtration and/or centrifugation and purifying the enzyme. The methods to purify the enzyme include conventional ones in general. From cultures intact cells and cell debris are eliminated and subjected to one or more methods such as concentration, salting out, dialysis, separatory sedimentation, gel filtration chromatography, ion-exchange chromatography, hydrophobic chromatography, affinity chromatography, gel electrophoresis and isoelectric point electrophoresis.

As is described above, the recombinant thermostable enzyme according to the present invention has a specific feature of releasing trehalose from non-reducing saccharides having a trehalose structure as an end unit and a degree of glucose polymerization of at least 3 even when allowed to act on them at a temperature exceeding 55°C. The trehalose thus obtained has a satisfactorily-mild and high-quality sweetness as well as an adequate viscosity and moisture-retaining ability, and, as a great advantageous feature, they can sweeten food products without fear of causing unsatisfactory coloration and deterioration because they have no reducing residue within their molecules. With these features a variety of amylaceous saccharides, which have been put aside because of their reducibilities, can be converted into saccharides which have a satisfactory handleability, usefulness, and no substantial reducibility or extremely-reduced reducibility.

Explaining now the conversion method in more detail, non-reducing saccharides having a trehalose structure and a degree of glucose polymerization of at least 3 such as α -glucosyltrehalose, α -maltosyltrehalose, α -maltotriosyltrehalose, α -maltotetraosyltrehalose and α -maltopentaosyltrehalose. These non-reducing saccharides can be obtained by allowing a non-reducing saccharide-forming enzyme as disclosed in Japanese Patent Application No.349,216/93, applied by the present applicant and Japanese Patent Application Serial No.10046601, titled "Thermostable non-reducing saccharide-forming enzyme, its preparation and uses", applied by the same applicant on June 24, 1994, to act on reducing amylaceous saccharides having a degree of glucose polymerization of at least 3 which are prepared by treating starch or amylaceous saccharides such as amylopectin and amylose with acids and/or amylases. These reducing saccharides usable as a substrate for the non-reducing saccharide-forming enzyme usually contain one or more maltooligosaccharides having a degree of glucose polymerization of at least 3, for example, maltotriose, maltotetraose, maltopentaose, maltohexaose and maltoheptaose. As is described in "Handbook of Amylases and Related Enzymes", 1st edition (1988), edited by The Amylase Research Society of Japan, published by Pergamon Press plc, Oxford, England, α -amylase, maltotetraose-forming amylase, maltopentaose-forming amylase and maltohexaose-forming amylase are especially useful to prepare the reducing amylaceous saccharides used in the present invention, and, the use of any one of these amylases facilitates the production of mixtures of amylaceous saccharides rich in reducing amylaceous saccharides having a degree of glucose polymerization of at least 3 in a considerably-high yield. If necessary, the combination use of the amylases and starch debranching enzymes such as pullulanase and isoamylase can increase the yield of the reducing amylaceous saccharides used as the substrate for the present recombinant thermostable enzyme. Non-reducing saccharides can be obtained in a desired amount by coexisting such a non-reducing saccharide-forming enzyme in aqueous solutions containing one or more reducing amylaceous saccharides up to 50 w/w %, and, usually,

incubating the mixture solution at a temperature of 40-85°C and a pH of about 4-8 until the non-reducing saccharides are produced.

In the enzymatic conversion method according to the present invention, the present recombinant thermostable enzyme is generally allowed to coexist in an aqueous solution containing one or more of the above non-reducing saccharides as a substrate, followed by the enzymatic reaction at a prescribed temperature and pH until a desired amount of trehalose is formed. Although the enzymatic reaction proceeds even at a concentration of about 0.1 w/w %, d.s.b., of a substrate, a concentration of 2 w/w % or higher, d.s.b., preferably, in the range of 5-50 w/w %, d.s.b., of a substrate can be satisfactorily used when used the present conversion method in an industrial-scale production. The temperature and pH used in the enzymatic reaction are set to within the range of which does not inactivate the recombinant thermostable enzyme and allows the enzyme to effectively act on substrates, i.e. a temperature of higher than 55°C but not higher than 85°C, preferably, a temperature in the range of about 56-70°C, and a pH of 4-7, preferably, a pH in the range of about 5-6. The amount and reaction time suitable for the present recombinant thermostable enzyme are chosen depending on the enzymatic reaction condition. Thus, the present recombinant thermostable enzyme effectively converts non-reducing saccharides having a trehalose structure as an end unit and a degree of glucose polymerization of at least 3 into trehalose and glucose and/or maltooligosaccharides, e.g. the conversion rate increases up to about 99% when the enzyme acts on α -maltotriosyltrehalose. When either of amylases is allowed to act on starch hydrolysates in combination with the non-reducing saccharide-forming enzyme and the present thermostable enzyme, non-reducing saccharides are formed along with trehalose and glucose and/or maltooligosaccharides. Thus, saccharide compositions rich in trehalose are efficiently formed in a relatively-high yield.

The reaction mixtures obtained by the present conversion reaction can be used intact, and, usually, they are purified prior to use. Insoluble substances are eliminated from the reaction mixtures by filtration and centrifugation, and the resultant solutions are decolored with activated charcoals, desalted and purified on ion exchangers, and concentrated into syrupy products. Depending on their use, the syrupy products are dried *in vacuo* and spray-dried into solid products. In order to obtain products which substantially consist of non-reducing saccharides, the aforesaid syrupy products are subjected to one or more methods such as chromatography using an ion exchanger, activated charcoal and silica gel for saccharide separation, separatory sedimentation using alcohol and/or acetone, membrane filtration, fermentation by yeasts, and removal and decomposition of reducing saccharides by alkalis. The methods to treat a relatively-large amount of a reaction mixture are, for example, fixed bed- or pseudomoving bed-ion exchange chromatography as disclosed in Japanese Patent Laid-Open Nos. 23,799/83 and 72,598/83, and such a method produces non-reducing saccharide-rich products on an industrial scale and in a considerably-high yield.

The trehalose and compositions containing it have a wide applicability to a variety of products which are apt to be readily damaged by the reducibility of saccharide sweeteners. For example, they can be satisfactorily used in food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant.

The following Examples explain in detail the preparation of the present recombinant thermostable enzyme, and the enzymatic conversion method of non-reducing saccharides:

Example A-1

Preparation of recombinant thermostable enzyme

In 500-ml flasks were placed about 100 ml aliquots of a liquid culture medium (pH 7.0) consisting of one w/v % polypeptone, 0.5 w/v % yeast extract, 0.5 w/v % sodium chloride, and water, and to each flask was sterilized by autoclaving at 120°C for 20 min, and admixed with 50 μ g/ml ampicillin. Thereafter, the flasks were cooled and inoculated with the transformant SU18 obtained by the method in Experiment 3-2, followed by the culture of the transformant at 37°C for 24 hours under a rotary shaking condition of 130 rpm to obtain a seed culture. To 30-L fermenter was placed about 18 L of a fresh preparation of the same liquid culture medium, sterilized similarly as above, cooled to 37°C, admixed with 50 μ g/ml ampicillin, and inoculated with one v/v % of the seed culture, followed by the culture at 37°C for 24 hours under aeration and agitation conditions.

The resultant culture was treated with ultrasonic to disrupt cells, and the resultant suspension was centrifuged to remove insoluble substances, followed by assaying the enzymatic activity in the supernatant to find that one L of the culture contained about 350 units of the present recombinant thermostable enzyme. The culture supernatant was purified by the method in Experiment 1 to obtain an about 12 ml aqueous solution containing about 230 units/ml of the present recombinant thermostable enzyme having a specific activity of about 720 units/mg protein.

Example A-2 (a)Preparation of transformant

5 Recombinant DNA pSU18 obtained by the method in Experiment 3-2 was cleaved with restriction enzymes *Ssp* I and *Ban* III to obtain a DNA fragment consisting of about 720 base pairs of a base sequence of bases 22 through 740 of SEQ ID NO:2. The DNA fragment was admixed with and ligated to "Bluescript II SK(+)", a plasmid vector commercialized by Pharmacia LKB Biotechnology AB, Uppsala, Sweden, which had been cleaved with restriction enzymes *Ssp* I and *Ban* III, at 4°C overnight in the presence of T4 DNA ligase to obtain a first recombinant DNA.

10 Five oligonucleotides, which were chemically synthesized in usual manner and had the following base sequences represented by 5'-CTGCAGTTTTTTAATAAAATCAGGAGGA-3', 5'-AAAAATATGTTTTCGTTTCGGTGGAAAT-3', 5'-ATT-TCCACCGAACGAAAA-3', CATATTTTTCTCCTCTGA-3', and 5'-TTTTATTAAAAAACTGCAG-3', were mixed in an appropriate ratio, and the mixture was successively incubated at 100°C, 65°C, 37°C and 20°C for each 20 min to anneal them. The resultant base sequence in SEQ ID NO:6 and a double strand DNA consisting of 55 base pairs of bases 1 through 21 of SEQ ID NO:6 were ligated similarly as above with the first recombinant DNA which had been cleaved with *Ssp* I as a restriction enzyme to obtain a second recombinant DNA having the base sequence in SEQ ID NO:6 and a base sequence of bases 1 through 740 of SEQ ID NO:2.

15 Recombinant DNA pSU18 obtained by the method in Experiment 3-2 was cleaved with restriction enzymes *Ban* III and *Bst* XI, and the resultant DNA fragment consisting of about 1,600 base pairs of a base sequence of bases 741 through 1,668 of SEQ ID NO:2 was ligated with "Bluescript II SK(+)", a plasmid vector which had been cleaved with restriction enzymes *Ban* III and *Bst* XI to obtain a third recombinant DNA.

20 Five oligonucleotides, which were chemically synthesized in usual manner, having the following base sequences represented by 5'-AACAGAGGTGTTGGG-3', 5'-GTATATCAATTAGAATGAAGCTT GAGCT-3', 5'-CAAGCTTCATTC-TA-3', and 5'-ATTGATATACCCCAACACCTCTGTT -3' were mixed in an appropriate ratio, and the mixture was annealed similarly as above. The resultant double strand DNA having the base sequence in SEQ ID NO:7 consisting of 40 base pairs of bases 1,639 through 1,668 of SEQ ID NO:2 was ligated to the third recombinant DNA which had been cleaved with restriction enzymes *Hpa* I and *Sac* I to obtain a fourth recombinant DNA having the base sequence in SEQ ID NO:7 and a base sequence of bases 741 through 1,668 of SEQ ID NO:2.

25 A DNA fragment which consists of about 770 base pairs, having a base sequence of bases 1 through 740 of SEQ ID NO:2, that had been obtained by cleaving the second recombinant DNA with restriction enzymes *Pst* I and *Ban* III, and a DNA fragment which consists of about 930 base pairs having a base sequence of bases 741 through 1,668 of SEQ ID NO:2, that had been obtained by cleaving the fourth recombinant DNA with restriction enzymes *Ban* III and *Hind* III, were ligated to "pKK223-3", which had been cleaved with restriction enzymes *Pst* I and *Hind* III, with T4 DNA ligase to obtain the present recombinant DNA pSU19 having the base sequence in SEQ ID NO:2.

30 In accordance with the method in Experiment 3-2, the recombinant DNA pSU19 was introduced into "BMH71-18", a competent cell commercialized by Takara Shuzo Co., Ltd., Tokyo, Japan, to obtain transformant SU19 having a DNA encoding the present recombinant thermostable enzyme. The transformant SU19 was cultured by the method in Experiment 3-2, and the proliferated cells were collected from the resultant culture. A recombinant DNA was extracted from the cells and analyzed and revealing that it consists of about 6,300 base pairs, and, as shown in FIG.6, it has a DNA consisting of 1,668 base pairs located in the downstream of the cleavage site of *Ssp* I, a restriction enzyme.

Example A-2 (b)Preparation of recombinant thermostable enzyme from transformant

35 The transformant SU19 in Example A-2 (a) was cultured similarly as in Example A-1 except that a liquid nutrient culture medium (pH 7.0) consisting of 2 w/v % maltose, 4 w/v % "N-Z-SOY PEPTONE commercialized by Sigma Chemicals Co., St. Louis, Missouri, USA, 2 w/v % yeast extract, 0.5 w/v % sodium dihydrogen phosphate, 50 µg/ml ampicillin, and water was used. The resultant culture was treated with ultrasonic to disrupt cells, and the cell suspension was centrifuged to remove insoluble substances, followed by assaying the recombinant thermostable enzyme activity in the resultant supernatant and revealing that one L culture yielded about 800,000 units of the objective recombinant thermostable enzyme. The supernatant was purified by the method in Experiment 1 to obtain an about 1,850 ml aqueous solution containing about 3,200 units/ml of the recombinant thermostable enzyme with a specific activity of about 720 units/mg protein.

40 The purified enzyme was assayed for properties and features by the method in Experiment 2 and revealing that it had a molecular weight of about 54,000-64,000 daltons on SDS-PAGE and a pI of about 5.6-6.6 on isoelectrophoresis, and was not substantially inactivated even when incubated in an aqueous solution (pH 7.0) at 85°C for 60 min. These physicochemical properties were substantially the same as those of the thermostable enzyme from a donor microor-

ganism of *Sulfolobus acidocaldarius* (ATCC 33909).

Example B-1 (a)

Conversion into syrupy product containing trehalose

To 500-ml flasks were added about 100 ml aliquots of a liquid culture medium consisting of 0.1 w/v % polypepton, 0.1 w/v % yeast extract, 0.2 w/v % ammonium sulfate, 0.05 w/v % potassium dihydrogen phosphate, 0.02 w/v % magnesium sulfate heptahydrate, 0.02 w/v % potassium chloride, and water. The flasks were sterilized by autoclaving at 120°C for 20 min, cooled and adjusted its pH to 3.0 by the addition of sulfuric acid. A seed culture of *Sulfolobus acidocaldarius* (ATCC 33909) was inoculated to the flasks, and cultured at 75°C for 24 hours under a rotatory shaking condition of 130 rpm to obtain a first seed culture. About 5 L of a fresh preparation of the same liquid culture medium was placed in a 10-L fermenter, sterilized similarly as above, cooled to 75°C, adjusted to pH 3.0, incubation at 75°C for 24 hours under an aeration condition of 500 ml/min to obtain a second seed culture. Thereafter, about 250 L of a fresh preparation of the same liquid culture medium in a 300-L fermenter, sterilized similarly as above, cooled to 75°C, and cultured under aeration and agitation conditions of 100 L/min for 42 hours.

About 170 L of the resultant culture was filtered with an SF membrane, and the filtrate was centrifuged to obtain wet cells, and about 258 g of which was suspended in 300 ml of 10 mM phosphate buffer (pH 7.0) and ultrasonicated to disrupt the cells. The cell debris thus obtained was centrifuged at 10,000 rpm for 30 min, and about 300 ml of the resultant supernatant was mixed with ammonium sulfate to give a saturation degree of 70 w/v %, allowed to stand at 4°C for 24 hours, and centrifuged at 10,000 rpm for 30 min. The precipitate was collected, dissolved in an adequate amount of 10 mM Tris-HCl buffer (pH 8.5), and dialyzed against a fresh preparation of the same buffer for 24 hours. Thereafter, the dialyzed solution was centrifuged at 10,000 rpm for 30 min to obtain an about 300 ml of a supernatant with an enzymatic activity.

The supernatant was fed to a column packed with about 360 ml of "DEAE-TOYOPEARL®", a gel for ion-exchange column chromatography commercialized by Tosoh Corporation, Tokyo, Japan, which had been previously equilibrated with 10 mM Tris-HCl buffer (pH 8.5), and fed with a linear gradient buffer ranging from 0 M to 0.3 M in 10 mM Tris-HCl buffer (pH 8.5). Fractions with an enzymatic activity, eluted at a concentration of about 0.1 M sodium chloride, were collected, pooled, and dialyzed for 10 hours against 10 mM Tris-HCl buffer (pH 8.5) containing one M ammonium sulfate. The dialyzed solution was centrifuged at 10,000 rpm for 30 min to remove insoluble substances, fed to a column packed with about 350 ml of "BUTYL-TOYOPEARL® 650", a gel for hydrophobic chromatography commercialized by Tosoh Corporation, Tokyo, Japan, which had been previously equilibrated with 10 mM Tris-HCl buffer (pH 8.5) containing one M ammonium sulfate, and fed with a linear gradient buffer ranging from 1 M to 0 M ammonium sulfate in 10 mM Tris-HCl buffer (pH 8.5).

Fractions with an enzymatic activity eluted at about 0.8 M ammonium sulfate were collected, pooled, dialyzed for 16 hours against 10 mM Tris-HCl buffer (pH 8.5) containing 0.2 M sodium chloride, and centrifuged at 10,000 rpm for 30 min to remove insoluble substances. The resultant supernatant was fed to a column packed with about 350 ml of "TOYOPEARL® HW-55", a gel for gel chromatography commercialized by Tosoh Corporation, Tokyo, Japan, which had been previously equilibrated with 10 mM Tris-HCl buffer (pH 8.5) containing 0.2 M sodium chloride. Fractions with an enzymatic activity were collected from the eluate, pooled, and dialyzed against 10 mM Tris-HCl buffer (pH 8.5) for 16 hours. The dialyzed solution was centrifuged to remove insoluble substances, and the supernatant was subjected to hydrophobic column chromatography using "MONO Q", a gel for ion-exchange chromatography commercialized by Pharmacia LKB Uppsala, Sweden, followed by feeding to the column with a linear gradient buffer ranging from 0 M to 0.2 M of sodium chloride in 10 mM Tris-HCl buffer (pH 8.5). The fractions eluted at about 0.1 M sodium chloride were collected and pooled for the production of trehalose. The purified non-reducing saccharide-forming enzyme thus obtained had a specific activity of about 81 units/mg protein, and the yield was about 0.24 units per one L of the culture.

Throughout the specification the activity of a non-reducing saccharide-forming enzyme is expressed by the value measured on the following assay: Place 4 ml of 50 mM acetate buffer (pH 5.5) containing as a substrate 1.25 w/v % maltopentaose in a test tube, add one ml of an adequately diluted enzyme solution to the test tube, and incubate the mixture solution at 60°C for 60 min to effect enzymatic reaction and heated at 100°C for 30 min to suspend the enzymatic reaction. Thereafter, one ml of the reaction mixture was diluted with deionized water by 10 times and assayed for reducing power on the Somogyi-Nelson's method. As a control, a system using an enzyme solution, which has been heated at 100°C for 30 min to inactivate the enzyme, is provided and similarly treated as above. One unit activity of the non-reducing saccharide-forming enzyme is defined as the amount of enzyme which diminishes the reducing power of one μ mol maltopentaose per min under the same conditions as mentioned above.

Example B-1 (b)Conversion into syrupy product containin trehalose

5 Corn starch was suspended in water into a 15 w/w % suspension which was then admixed with 0.1 w/w % calcium carbonate. Th mixture was adjusted to pH 6.0, admixed with 0.2 w/w % of "TERMAMYL 60L", an α -amylase specimen commercialized by Novo Nordisk Bioindustri A/S, Copenhagen, Denmark, to starch, d.s.b., and enzymatically reacted at 95°C for 15 hours to gelatinize and liquefy the starch. The reaction mixture was autoclaved at 120°C for 30 min to inactivate the remaining enzyme, cooled to 58°C, adjusted to pH 5.5, admixed with 3,000 units/g starch, d.s.b., of an isoamylase specimen, 3.0 units/g starch, d.s.b., of a recombinant thermostable enzyme obtained by the method in Example B-1 (a), and 5.0 units/starch, d.s.b., of a recombinant thermostable enzyme obtained by the method in Example A-1, and enzymatically reacted for 64 hours. The resultant reaction mixture was heated at 97°C for 30 min to inactivate the remaining enzyme, cooled and filtered, and the resultant filtrate was in usual manner decolored with an activated charcoal, desalted and purified with an ion exchanger and concentrated to obtain an about 60 w/w % syrup in a yield of about 90% to the material starch, d.s.b.

15 The syrup had a relatively-low DE (dextrose equivalent) and contained 71.0 w/w % trehalose, 2.9 w/w % glucosyl-trehalose, 1.0 w/w % maltosyltrehalose, 4.9 w/w % glucose, 10.5 w/w % maltose, 8.2 w/w % maltotriose and 1.5 w/w % maltotetraose and higher maltooligosaccharides, d.s.b. The product, having a mild and moderate sweetness as well as an adequate viscosity and moisture-retaining ability, can be satisfactorily used in compositions in general such as food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant.

Example B-2Conversion into powdery product containing trehalose

25 A syrupy product in Example B-1 was column chromatographed using a strong-acid cation exchange resin to increase the trehalose content. The procedures were as follows: Four jacketed-stainless steel columns, 5.4 cm in diameter and 5 m in length each, were packed to homogeneity with "XT-1016 (Na⁺-form)", a strong-acid cation exchange resin commercialized by Tokyo Organic Chemical Industries, Ltd., Tokyo, Japan, which had been previously suspended in water, and cascaded in series to give a total column length of 20 m. The columns were fed with the syrupy product, adequately diluted with water, in a volume of about 5 v/v % to the resin and at an inner column temperature of 55°C, and fed with 55°C hot water at an SV (space velocity) 0.13 to elute saccharide components. Fractions rich in trehalose were collected, pooled, concentrated, dried *in vacuo* and pulverized to obtain a powdery product containing about 97 w/w % trehalose in a yield of about 55 w/w % to the material, d.s.b.

35 The product has a mild and moderate sweetness as well as no substantial reducibility, and can be satisfactorily used in compositions in general such as food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant.

Example B-3Conversion into syrupy product containing non-reducing saccharide

45 A fraction rich in trehalose obtained by the method in Example B-2 was concentrated into an about 75 w/w % solution which was then transferred to a crystallizer, and crystallized under gently stirring conditions to obtain a masseccuite with a crystallization percentage of about 45 w/w %, d.s.b. The masseccuite was sprayed downward from a nozzle equipped on the upper part of a spraying tower at a pressure of about 150 kg/cm² while an about 85°C hot air was blowing downward from the upper part of the spraying tower, and the formed crystalline powder was collected on a wire-netting conveyer provided on the basement of the drying tower and gradually conveyed out of the spraying tower while an about 45°C hot air was blowing to the crystalline powder from under the conveyer. The crystalline powder thus obtained was transferred to an ageing tower and aged for 10 hours in a stream of about 40°C hot air to complete the crystallization and drying. Thus, a powdery hydrous crystalline trehalose was obtained in a yield of about 90 w/w % to the material, d.s.b.

55 The product has a mild and high-quality sweetness as well as substantial no hygroscopicity, and can be suitably incorporated into compositions in general such as food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient, and adjuvant.

Example B-4Conversion into powdery product containing crystalline trehalose

5 Tapioca starch was dissolved in water into a 36 w/w % suspension which was then admixed with 0.1 w/w % calcium carbonate. The mixture was adjusted to pH 6.0, admixed with 0.2 w/w % of "TERMAMYL 60L", an α -amylase specimen commercialized by Novo Nordisk Bioindustri A/S, Copenhagen, Denmark, to starch, d.s.b., and enzymatically reacted at 95°C for 15 min to gelatinize and liquefy the starch. The mixture was autoclaved at 120°C for 30 min to inactivate the remaining enzyme, cooled to 58°C, adjusted to pH 5.2, admixed with 2,000 units/g starch, d.s.b., of an isoamylase
 10 specimen commercialized by Hayashibara Biochemical Laboratories, Inc., Okayama, Japan, 2.5 units/g starch, d.s.b., of a thermostable enzyme obtained by the method in Example B-1 (a), 5.0 units/g starch, d.s.s.b. of a recombinant thermostable enzyme obtained by the method in Example A-1, and subjected to an enzymatic reaction for 72 hours. The reaction mixture was heated at 97°C for 30 min to inactivate the remaining enzyme, cooled to 50°C, admixed with 10 units/g starch, d.s.b., of "GLUCOZYME", Nagase Biochemicals, Ltd., Kyoto, Japan, and subjected to an enzymatic
 15 reaction for 40 hours. The reaction mixture thus obtained was heated at 95°C for 10 min to inactivate the remaining enzyme, cooled, filtered, decolored in usual manner with an activated charcoal, desalted and purified with ion exchangers, and concentrated into an about 60 w/w % syrup to obtain a syrupy product containing about 75.5 w/w % trehalose, d.s.b.

20 The syrupy product was concentrated into an about 84 w/w % solution which was then transferred to a crystallizer, admixed with about 2 w/w %, d.s.b., of hydrous crystalline trehalose as a seed crystal, and crystallized under gentle stirring conditions to obtain a massecuite with a crystallization percentage of about 45 w/w %, d.s.b. The massecuite was distributed to plastic plane vessels, allowed to stand at ambient temperature for 3 days to solidify and age the contents. Thereafter, the formed blocks were removed from the vessels, powdered by a pulverizer to obtain a solid product containing hydrous crystalline trehalose in a yield of about 90 w/w % to the material starch, d.s.b.

25 The product has a mild and high-quality sweetness as well as substantial no hygroscopicity, and can be suitably incorporated into compositions in general such as food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient, and adjuvant.

Example B-5Conversion into powder product containing crystalline trehalose

30 Potato starch was suspended in water into a 6 w/w % suspension which was then admixed with 0.01 w/w % "NEO-SPITASE", an α -amylase specimen commercialized by Nagase Biochemicals, Ltd., Kyoto, Japan, adjusted to pH 6.2, and subjected to an enzymatic reaction at a temperature of 85-90°C for one hour to gelatinize and liquefy the starch. The mixture was heated at 120°C for 10 min to inactivate the remaining enzyme, cooled to 60°C, adjusted to pH 5.5, admixed with 500 units/g starch, d.s.b., of "PROMOZYME 200L", a pullulanase specimen commercialized by Novo Nordisk Bioindustri A/S, Copenhagen, Denmark, 3.0 units/g starch, d.s.b., of a thermostable non-reducing saccharide-forming enzyme obtained by the method in Example B-1 (a), 5.0 units/g starch, d.s.b., of a recombinant thermostable
 40 enzyme obtained by the method in Example A-1, and subjected to an enzymatic reaction for 48 hours. The reaction mixture was heated at 97°C for 30 min to inactivate the remaining enzyme, adjusted to 50°C and to pH 5.0, admixed with 10 units/g starch, d.s.b., of "GLUCOZYME", Nagase Biochemicals, Ltd., Kyoto, Japan, and subjected to an enzymatic reaction for 40 hours. The reaction mixture thus obtained was heated at 95°C for 10 min to inactivate the remaining enzyme, cooled, filtered, decolored in usual manner with an activated charcoal, desalted and purified with ion exchangers, and concentrated into an about 60 w/w % syrup to obtain a syrupy product containing about 79.3 w/w % trehalose, d.s.b.

45 The syrupy product was column chromatographed similarly as in Example B-2 except that "C6000", commercialized by Japan Organo Co., Ltd., Tokyo, Japan, was used a strong-acid cation exchange resin in Na⁺-form, followed by collecting a fraction containing about 95 w/w % trehalose, d.s.b. The fraction was concentrated up to about 75 w/w % and crystallized similarly as in Example B-4 to obtain a massecuite in the form of block which was then pulverized to obtain a powdery product containing hydrous crystalline trehalose in a yield of about 70 w/w % to the material starch, d.s.b.

50 The product is substantially free of hygroscopicity and readily handleable, and can be suitably incorporated into compositions in general such as food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient, and adjuvant.

Example B-6Conversion into powdery product containing anhydrous crystalline trehalose

One part by weight of "EX-I", an amylose product commercialized by Hayashibara Biochemical Laboratories, Inc., Okayama, Japan, was dissolved by heating in 15 parts by weight of water, and the solution was adjusted to 65°C and pH 5.5, admixed with 2.0 units/g amylose, d.s.b., of a thermostable non-reducing saccharide-forming enzyme obtained by the method in Example B-1 (a) and 6.0 units/g amylose, d.s.b., of a recombinant thermostable enzyme obtained by the method in Example A-2, and subjected to an enzymatic reaction for 48 hours. The reaction mixture was incubated at 97°C for 30 min to inactivate the remaining enzyme, adjusted to 50°C and pH 5.0, admixed with 10 units/g amylose, d.s.b., "GLUCOZYME", a glucoamylase specimen commercialized by Nagase Biochemicals, Ltd., Kyoto, Japan, and incubated for another 40 hours. The newly formed reaction mixture was heated at 95°C for 10 min to inactivate the remaining enzyme, cooled, filtered in usual manner, decolorized with an activated charcoal, deionized and purified with an ion exchanger, and concentrated up to give a concentration of about 60 w/w % to obtain a syrupy product containing 82.2 w/w % trehalose, d.s.b.

The syrupy product was similarly as in Example B-5 subjected to column fractionation to obtain a fraction containing 98 w/w % trehalose, d.s.b., which was then concentrated by heating under a reduced pressure up to give a concentration of about 85 w/w %. To the concentrate was added about 2 w/w % anhydrous crystalline trehalose as a seed, followed by mixing the resultant at 120°C for 5 min under stirring conditions. The resultant mixture was distributed to plastic plain vessels, and crystallized by drying *in vacuo* at 100°C. Thereafter, products in the form of a block were removed from the vessels, pulverized with a cutter to obtain a solid product, which contained anhydrous crystalline trehalose and had a moisture content of about 0.3 w/w % and a crystallization percentage of about 70 w/w %, in a yield of about 70% to the material amylose, d.s.b.

Anhydrous crystalline trehalose absorbs moisture from anhydrous substances to convert into hydrous crystalline trehalose, and because of this the product rich in such anhydrous crystalline trehalose is useful as a desiccant to dehydrate compositions such as food products, cosmetics and pharmaceuticals, and their materials and intermediates. The product with a mild and high-quality sweetness can be arbitrarily incorporated into compositions in general such as food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, diluent and excipient.

As is described above, the present invention is based on the finding of a novel thermostable enzyme which releases trehalose from non-reducing saccharides having a trehalose structure as an end unit and a degree of glucose polymerization of at least 3. The present invention is to explore a way to produce such a thermostable enzyme in an industrial scale and in a relatively-high efficiency by the recombinant DNA technology. The present conversion method using the recombinant thermostable enzyme readily converts non-reducing amylaceous saccharides, which have a trehalose structure as an end unit and a degree of glucose polymerization of at least 3, into trehalose and glucose and/or maltoligosaccharides without fear of causing bacterial contamination. The trehalose has a mild and high-quality sweetness, and, because it has no reducing residue within the molecule, it can be advantageously incorporated into compositions in general such as food products, cosmetics and pharmaceuticals without fear of causing unsatisfactory coloration and deterioration. The present recombinant thermostable enzyme is one which has a revealed amino acid sequence, so that it can be used freely in the preparation of trehalose that is premised to be used in food products and pharmaceuticals.

Thus, the present invention is a significant invention which exerts the aforesaid satisfactory effects and greatly contributes to this field.

While there has been described what is at present considered to be the preferred embodiments of the invention, it will be understood that various modifications may be made therein, and it is intended to cover in the appended claims all such modifications as fall within the true spirit and scope of the invention.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
KENKYUJO
(B) STREET: 2-3, 1-CHOME, SHIMOISHII
(C) CITY: OKAYAMA
(E) COUNTRY: JAPAN
(F) POSTAL CODE (ZIP): 700

(ii) TITLE OF INVENTION: RECOMBINANT THERMOSTABLE ENZYME WHICH
RELEASES TREHALOSE FROM NON-REDUCING
SACCHARIDE

(iii) NUMBER OF SEQUENCES: 8

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(v) CURRENT APPLICATION DATA:

APPLICATION NUMBER: EP 95305100.0

(vi) PRIOR APPLICATION DATA:

(A1) APPLICATION NUMBER: JP 190180/94
(B1) FILING DATE: July 21, 1994
(A2) APPLICATION NUMBER: JP 109128/95
(B2) FILING DATE: April 11, 1995
(A3) APPLICATION NUMBER: JP 189760/95
(B3) FILING DATE: July 4, 1995

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 556 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Phe	Ser	Phe	Gly	Gly	Asn	Ile	Glu	Lys	Asn	Lys	Gly	Ile	Phe	1	5	10	15
Lys	Leu	Trp	Ala	Pro	Tyr	Val	Asn	Ser	Val	Lys	Leu	Lys	Leu	Ser	20	25	30	35
Lys	Lys	Leu	Ile	Pro	Met	Glu	Lys	Asn	Asp	Glu	Gly	Phe	Phe	Glu	40	45	50	55
Val	Glu	Ile	Asp	Asp	Ile	Glu	Glu	Asn	Leu	Thr	Tyr	Ser	Tyr	Ile	60	65	70	75
Ile	Glu	Asp	Lys	Arg	Glu	Ile	Pro	Asp	Pro	Ala	Ser	Arg	Tyr	Gln	80	85	90	95
Pro	Leu	Gly	Val	His	Asp	Lys	Ser	Gln	Leu	Ile	Arg	Thr	Asp	Tyr	100	105	110	115
Gln	Ile	Leu	Asp	Leu	Gly	Lys	Val	Lys	Ile	Glu	Asp	Leu	Ile	Ile	120	125	130	135
Tyr	Glu	Leu	His	Val	Gly	Thr	Phe	Ser	Gln	Glu	Gly	Asn	Phe	Lys	140	145	150	155
Gly	Val	Ile	Glu	Lys	Leu	Asp	Tyr	Leu	Lys	Asp	Leu	Gly	Ile	Thr	160	165	170	175
Gly	Ile	Glu	Leu	Met	Pro	Val	Ala	Gln	Phe	Pro	Gly	Asn	Arg	Asp	180	185	190	195

		140		145		150
	Trp Gly Tyr Asp	Gly Val Phe Leu Tyr	Ala Val Gln Asn Thr Tyr			
		155		160		165
5	Gly Gly Pro Trp	Glu Leu Ala Lys Leu	Val Asn Glu Ala His Lys			
		170		175		180
	Arg Gly Ile Ala	Val Ile Leu Asp Val	Val Tyr Asn His Ile Gly			
		185		190		195
	Pro Glu Gly Asn	Tyr Leu Leu Gly Leu	Gly Pro Tyr Phe Ser Asp			
		200		205		210
10	Arg Tyr Lys Thr	Pro Trp Gly Leu Thr	Phe Asn Phe Asp Asp Arg			
		215		220		225
	Gly Cys Asp Gln	Val Arg Lys Phe Ile	Leu Glu Asn Val Glu Tyr			
		230		235		240
	Trp Phe Lys Thr	Phe Lys Ile Asp Gly	Leu Arg Leu Asp Ala Val			
		245		250		255
15	His Ala Ile Phe	Asp Asn Ser Pro Lys	His Ile Leu Gln Glu Ile			
		260		265		270
	Ala Glu Lys Ala	His Gln Leu Gly Lys	Phe Val Ile Ala Glu Ser			
		275		280		285
	Asp Leu Asn Asp	Pro Lys Ile Val Lys	Asp Asp Cys Gly Tyr Lys			
		290		295		300
20	Ile Asp Ala Gln	Trp Val Asp Asp Phe	His His Ala Val His Ala			
		305		310		315
	Phe Ile Thr Lys	Glu Lys Asp Tyr Tyr	Tyr Gln Asp Phe Gly Arg			
		320		325		330
	Ile Glu Asp Ile	Glu Lys Thr Phe Lys	Asp Val Phe Val Tyr Asp			
		335		340		345
25	Gly Lys Tyr Ser	Arg Tyr Arg Gly Arg	Thr His Gly Ala Pro Val			
		350		355		360
	Gly Asp Leu Pro	Pro Arg Lys Phe Val	Val Phe Ile Gln Asn His			
		365		370		375
	Asp Gln Val Gly	Asn Arg Gly Asn Gly	Glu Arg Leu Ser Ile Leu			
		380		385		390
30	Thr Asp Lys Thr	Thr Tyr Leu Met Ala	Ala Thr Leu Tyr Ile Leu			
		395		400		405
	Ser Pro Tyr Ile	Pro Leu Ile Phe Met	Gly Glu Glu Tyr Tyr Glu			
		410		415		420
	Thr Asn Pro Phe	Phe Phe Phe Ser Asp	Phe Ser Asp Pro Val Leu			
		425		430		435
35	Ile Lys Gly Val	Arg Glu Gly Arg Leu	Lys Glu Asn Asn Gln Met			
		440		445		450
	Ile Asp Pro Gln	Ser Glu Glu Ala Phe	Leu Lys Ser Lys Leu Ser			
		455		460		465
	Trp Lys Ile Asp	Glu Glu Val Leu Asp	Tyr Tyr Lys Gln Leu Ile			
		470		475		480
40	Asn Ile Arg Lys	Arg Tyr Asn Asn Cys	Lys Arg Val Lys Glu Val			
		485		490		495
	Arg Arg Glu Gly	Asn Cys Ile Thr Leu	Ile Met Glu Lys Ile Gly			
		500		505		510
	Ile Ile Ala Ser	Phe Asp Asp Ile Val	Ile Asn Ser Lys Ile Thr			
		515		520		525
45	Gly Asn Leu Leu	Ile Gly Ile Gly Phe	Pro Lys Lys Leu Lys Lys			
		530		535		540
	Asp Glu Leu Ile	Lys Val Asn Arg Gly	Val Gly Val Tyr Gln Leu			
		545		550		555
	Glu					

(3) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1668 base pairs

(B) TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGTTTTTCGT TCGGTGGAAA TATTGAAAAA AATAAAGGTA TCTTTAAGTT ATGGGCACCT 60
 TATGTTAATA GTGTTAAGCT GAAGTTAAGC AAAAAACTTA TTCCAATGGA AAAAAACGAT 120
 GAGGGATTTT TCGAAGTAGA AATAGACGAT ATCGAGGAAA ATTTAACCTA TTCTTATATT 180
 ATAGAAGATA AGAGAGAGAT ACCTGATCCC GCATCACGAT ATCAACCTTT AGGAGTTCAT 240
 5 GACAAATCAC AACTTATAAG AACAGATTAT CAGATTCTTG ACCTTGGAAA AGTAAAAATA 300
 GAAGATCTAA TAATATATGA ACTCCACGTT GGTACTTTTTT CCCAAGAAGG AAATTTCAAA 360
 GGAGTAATAG AAAAGTTAGA TTACCTCAAG GATCTAGGAA TCACAGGAAT TGAAGTATG 420
 CCTGTGGCAC AATTTCAGG GAATAGAGAT TGGGGATACG ATGGTGTTTT TCTATACGCA 480
 GTTCAAATA CTTATGGCGG ACCATGGGAA TTGGCTAAGC TAGTAAACGA GGCACATAAA 540
 AGGGGAATAG CCGTAATTTT GGATGTTGTA TATAATCATA TAGGTCCTGA GGGAAATTAC 600
 10 CTTTTAGGAT TAGGTCCTTA TTTTTCAGAC AGATATAAAA CTCCATGGGG ATTAACATTT 660
 AATTTTGATG ATAGGGGATG TGATCAAGTT AGAAAATTCA TTTTAGAAAA TGTCGAGTAT 720
 TGGTTTAAGA CTTTAAAT CGATGGTCTG AGACTGGATG CAGTTCATGC AATTTTTGAT 780
 AATTCGCCTA AGCATATCCT CCAAGAGATA GCTGAAAAAG CCCATCAATT AGGAAAATTT 840
 GTTATTGCTG AAAGTGATT AAATGATCCA AAAATAGTAA AAGATGATTG TGGATATAAA 900
 ATAGATGCTC AATGGGTTGA CGATTTCCAC CACGCAAGTC ATGCATTAT AACCAGAA 960
 15 AAAGATTATT ATTACCAGGA TTTTGGAAGG ATAGAAGATA TAGAGAAAAC TTTTAAAGAT 1020
 GTTTTTGTTT ATGATGGAAA GTATTCTAGA TACAGAGGAA GAACTCATGG TGCTCCTGTA 1080
 GGTGATCTTC CACCACGTAA ATTTGTAGTC TTCATACAAA ATCACGATCA AGTAGGAAAT 1140
 AGAGGAAATG GGGAAAGACT TTCCATATTA ACCGATAAAA CGACATACCT TATGGCAGCC 1200
 ACATATATA TACTCTCACC GTATATACCG CTAATATTTA TGGGCGAGGA ATATTATGAG 1260
 20 ACGAATCCTT TTTTCTTCTT CTCTGATTTT TCAGATCCCG TATTAATTAA GGGTGTAGA 1320
 GAAGGTAGAC TAAAGGAAAA TAATCAAATG ATAGATCCAC AATCTGAGGA AGCGTCTTA 1380
 AAGAGTAAAC TTTTATGGAA AATTGATGAG GAAGTTTTAG ATTATTATAA ACAACTGATA 1440
 AATATCAGAA AGAGATATAA TAATTGTAAA AGGGTAAAGG AAGTTAGGAG AGAAGGGAAC 1500
 TGTATTACTT TGATCATGGA AAAAATAGGA ATAATTGCAT CGTTTGATGA TATTGTAAAT 1560
 25 AATTCTAAAA TTACAGGTAA TTTACTTATA GGCATAGGAT TTCCGAAAAA ATTGAAAAAA 1620
 GATGAATTAA TTAAGGTTAA CAGAGGTGTT GGGGTATATC AATTAGAA 1668

(4) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:30 amino acids
 (B) TYPE:amino acid
 (D) TOPOLOGY:linear

(ii) MOLECULE TYPE:peptide

(v) FRAGMENT TYPE:N-terminal fragment

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:3:

Met Phe Ser Phe Gly Gly Asn Ile Glu Lys Asn Lys Gly Ile Phe
 1 5 10 15
 Lys Leu Trp Ala Pro Tyr Val Asn Ser Val Lys Leu Lys Leu Ser
 20 25 30

(5) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:19 amino acids
 (B) TYPE:amino acid
 (D) TOPOLOGY:linear

(ii) MOLECULE TYPE:peptide

(v) FRAGMENT TYPE:internal fragment

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:4:

Ile Asp Ala Gln Trp Val Asp Asp Phe His His Ala Val His Ala
 1 5 10 15
 Phe Ile Thr Lys

(6) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1668 base pairs

(B) TYPE: nucleic acid

(C) strandedness: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Sulfolobus acidocaldarius*

(B) INDIVIDUAL ISOLATE: ATCC 33909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

5	ATG TTT TCG TTC GGT GGA AAT ATT GAA AAA AAT AAA GGT ATC TTT AAG	48
	Met Phe Ser Phe Gly Gly Asn Ile Glu Lys Asn Lys Gly Ile Phe Lys	
10	1 5 10 15	
15	TTA TGG GCA CCT TAT GTT AAT AGT GTT AAG CTG AAG TTA AGC AAA AAA	96
	Leu Trp Ala Pro Tyr Val Asn Ser Val Lys Leu Lys Leu Ser Lys Lys	
20	20 25 30	
	CTT ATT CCA ATG GAA AAA AAC GAT GAG GGA TTT TTC GAA GTA GAA ATA	144
	Leu Ile Pro Met Glu Lys Asn Asp Glu Gly Phe Phe Glu Val Glu Ile	
25	35 40 45	
	GAC GAT ATC GAG GAA AAT TTA ACC TAT TCT TAT ATT ATA GAA GAT AAG	192
	Asp Asp Ile Glu Glu Asn Thr Tyr Ser Tyr Ile Ile Glu Asp Lys	
30	50 55 60	
	AGA GAG ATA CCT GAT CCC GCA TCA CGA TAT CAA CCT TTA GGA GTT CAT	240
	Arg Glu Ile Pro Asp Pro Ala Ser Arg Tyr Gln Pro Leu Gly Val His	
35	65 70 75 80	
	GAC AAA TCA CAA CTT ATA AGA ACA GAT TAT CAG ATT CTT GAC CTT GGA	288
	Asp Lys Ser Gln Leu Ile Arg Thr Asp Tyr Gln Ile Leu Asp Leu Gly	
40	85 90 95	
	AAA GTA AAA ATA GAA GAT CTA ATA ATA TAT GAA CTC CAC GTT GGT ACT	336
	Lys Val Lys Ile Glu Asp Leu Ile Ile Tyr Glu Leu His Val Gly Thr	
45	100 105 110	
	TTT TCC CAA GAA GGA AAT TTC AAA GGA GTA ATA GAA AAG TTA GAT TAC	384
	Phe Ser Gln Glu Gly Asn Phe Lys Gly Val Ile Glu Lys Leu Asp Tyr	
50	115 120 125	
	CTC AAG GAT CTA GGA ATC ACA GGA ATT GAA CTG ATG CCT GTG GCA CAA	432
	Leu Lys Asp Leu Gly Ile Thr Gly Ile Glu Leu Met Pro Val Ala Gln	
55	130 135 140	
	TTT CCA GGG AAT AGA GAT TGG GGA TAC GAT GGT GTT TTT CTA TAC GCA	480
	Phe Pro Gly Asn Arg Asp Trp Gly Tyr Asp Gly Val Phe Leu Tyr Ala	
60	145 150 155 160	
	GTT CAA AAT ACT TAT GGC GGA CCA TGG GAA TTG GCT AAG CTA GTA AAC	528
	Val Gln Asn Thr Tyr Gly Gly Pro Trp Glu Leu Ala Lys Leu Val Asn	
65	165 170 175	
	GAG GCA CAT AAA AGG GGA ATA GCC GTA ATT TTG GAT GTT GTA TAT AAT	576
	Glu Ala His Lys Arg Gly Ile Ala Val Ile Leu Asp Val Val Tyr Asn	
70	180 185 190	
	CAT ATA GGT CCT GAG GGA AAT TAC CTT TTA GGA TTA GGT CCT TAT TTT	624
	His Ile Gly Pro Glu Gly Asn Tyr Leu Leu Gly Leu Gly Pro Tyr Phe	
75	195 200 205	
	TCA GAC AGA TAT AAA ACT CCA TGG GGA TTA ACA TTT AAT TTT GAT GAT	672
	Ser Asp Arg Tyr Lys Thr Pro Trp Gly Leu Thr Phe Asn Phe Asp Asp	
80	210 215 220	
	AGG GGA TGT GAT CAA GTT AGA AAA TTC ATT TTA GAA AAT GTC GAG TAT	720
	Arg Gly Cys Asp Gln Val Arg Lys Phe Ile Leu Glu Asn Val Glu Tyr	
85	225 230 235 240	
	TGG TTT AAG ACC TTT AAA ATC GAT GGT CTG AGA CTG GAT GCA GTT CAT	768
	Trp Phe Lys Thr Phe Lys Ile Asp Gly Leu Arg Leu Asp Ala Val His	
90	245 250 255	
	GCA ATT TTT GAT AAT TCG CCT AAG CAT ATC CTC CAA GAG ATA GCT GAA	816
	Ala Ile Phe Asp Asn Ser Pro Lys His Ile Leu Gln Glu Ile Ala Glu	
95	260 265 270	
	AAA GCC CAT CAA TTA GGA AAA TTT GTT ATT GCT GAA AGT GAT TTA AAT	864
	Lys Ala His Gln Leu Gly Lys Phe Val Ile Ala Glu Ser Asp Leu Asn	

		275				280				285							
	GAT	CCA	AAA	ATA	GTA	AAA	GAT	GAT	TGT	GGA	TAT	AAA	ATA	CAT	GCT	C4A	912
5	Asp	Pro	Lys	Ile	Val	Lys	Asp	Asp	Cys	Gly	Tyr	Lys	Ile	Asp	Ala	Gln	
		290					295					300					
	TGG	GTT	GAC	GAT	TTC	CAC	CAC	GCA	GTT	CAT	GCA	TTC	ATA	ACC	AAA	GAA	960
	Trp	Val	Asp	Asp	Phe	His	His	Ala	Val	His	Ala	Phe	Ile	Thr	Lys	Glu	
		305				310					315					320	
	AAA	GAT	TAT	TAT	TAC	CAG	GAT	TTT	GGA	AGG	ATA	GAA	GAT	ATA	GAG	AAA	1008
10	Lys	Asp	Tyr	Tyr	Tyr	Gln	Asp	Phe	Gly	Arg	Ile	Glu	Asp	Ile	Glu	Lys	
					325					330					335		
	ACT	TTT	AAA	GAT	GTT	TTT	GTT	TAT	GAT	GGA	AAG	TAT	TCT	AGA	TAC	AGA	1056
	Thr	Phe	Lys	Asp	Val	Phe	Val	Tyr	Asp	Gly	Lys	Tyr	Ser	Arg	Tyr	Arg	
					340					345					350		
	GGA	AGA	ACT	CAT	GGT	GCT	CCT	GTA	GGT	GAT	CTT	CCA	CCA	CGT	AAA	TTT	1104
15	Gly	Arg	Thr	His	Gly	Ala	Pro	Val	Gly	Asp	Leu	Pro	Pro	Arg	Lys	Phe	
			355						360				365				
	GTA	GTC	TTC	ATA	CAA	AAT	CAC	GAT	CAA	GTA	GGA	AAT	AGA	GGA	AAT	GGG	1152
	Val	Val	Phe	Ile	Gln	Asn	His	Asp	Gln	Val	Gly	Asn	Arg	Gly	Asn	Gly	
			370				375					380					
	GAA	AGA	CTT	TCC	ATA	TTA	ACC	GAT	AAA	ACG	ACA	TAC	CTT	ATG	GCA	GCC	1200
20	Glu	Arg	Leu	Ser	Ile	Leu	Thr	Asp	Lys	Thr	Thr	Tyr	Leu	Met	Ala	Ala	
			385				390					395				400	
	ACA	CTA	TAT	ATA	CTC	TCA	CCG	TAT	ATA	CCG	CTA	ATA	TTT	ATG	GGC	GAG	1248
	Thr	Leu	Tyr	Ile	Leu	Ser	Pro	Tyr	Ile	Pro	Leu	Ile	Phe	Met	Gly	Glu	
					405					410					415		
	GAA	TAT	TAT	GAG	ACG	AAT	CCT	TTT	TTC	TTC	TTC	TCT	GAT	TTC	TCA	GAT	1296
25	Glu	Tyr	Tyr	Glu	Thr	Asn	Pro	Phe	Phe	Phe	Phe	Ser	Asp	Phe	Ser	Asp	
				420					425					430			
	CCC	GTA	TTA	ATT	AAG	GGT	GTT	AGA	GAA	GGT	AGA	CTA	AAG	GAA	AAT	AAT	1344
	Pro	Val	Leu	Ile	Lys	Gly	Val	Arg	Glu	Gly	Arg	Leu	Lys	Glu	Asn	Asn	
			435					440					445				
	CAA	ATG	ATA	GAT	CCA	CAA	TCT	GAG	GAA	GCG	TTC	TTA	AAG	AGT	AAA	CTT	1392
30	Gln	Met	Ile	Asp	Pro	Gln	Ser	Glu	Glu	Ala	Phe	Leu	Lys	Ser	Lys	Leu	
			450				455					460					
	TCA	TGG	AAA	ATT	GAT	GAG	GAA	GTT	TTA	GAT	TAT	TAT	AAA	CAA	CTG	ATA	1440
	Ser	Trp	Lys	Ile	Asp	Glu	Glu	Val	Leu	Asp	Tyr	Tyr	Lys	Gln	Leu	Ile	
			465			470					475				480		
	AAT	ATC	AGA	AAG	AGA	TAT	AAT	AAT	TGT	AAA	AGG	GTA	AAG	GAA	GTT	AGG	1488
35	Asn	Ile	Arg	Lys	Arg	Tyr	Asn	Asn	Cys	Lys	Arg	Val	Lys	Glu	Val	Arg	
				485						490					495		
	AGA	GAA	GGG	AAC	TGT	ATT	ACT	TTG	ATC	ATG	GAA	AAA	ATA	GGA	ATA	ATT	1536
	Arg	Glu	Gly	Asn	Cys	Ile	Thr	Leu	Ile	Met	Glu	Lys	Ile	Gly	Ile	Ile	
			500						505					510			
	GCA	TCG	TTT	GAT	GAT	ATT	GTA	ATT	AAT	TCT	AAA	ATT	ACA	GGT	AAT	TTA	1584
40	Ala	Ser	Phe	Asp	Asp	Ile	Val	Ile	Asn	Ser	Lys	Ile	Thr	Gly	Asn	Leu	
			515					520						525			
	CTT	ATA	GGC	ATA	GGA	TTT	CCG	AAA	AAA	TTG	AAA	AAA	GAT	GAA	TTA	ATT	1632
	Leu	Ile	Gly	Ile	Gly	Phe	Pro	Lys	Lys	Leu	Lys	Lys	Asp	Glu	Leu	Ile	
		530					535					540					
	AAG	GTT	AAC	AGA	GGT	GTT	GGG	GTA	TAT	CAA	TTA	GAA					1668
45	Lys	Val	Asn	Arg	Gly	Val	Gly	Val	Tyr	Gln	Leu	Glu					
		545				550					555						

(7) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTGCAGTTTT TTAATAAAAT CAGGAGGAAA AAAT

5

(8) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:13 base pairs

(B) TYPE:nucleic acid

(D) TOPOLOGY:linear

10

(ii) MOLECULE TYPE:synthesized DNA

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION:1..9

(D) OTHER INFORMATION:

/note= "Complementary with positions 1 to 9 of sequence 8"

15

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:7:

TGAAGCTTGA GCT

13

20

(9) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:9 base pairs

(B) TYPE:nucleic acid

(D) TOPOLOGY:linear

25

(ii) MOLECULE TYPE:synthesized DNA

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION:1..9

(D) OTHER INFORMATION:

/note= "Presented as 3' to 5' sequence complementary with positions 1 to 9 of sequence 7"

30

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:8:

ACTTCGAAC

9

35

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45

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55

SEQUENCE LISTING

(1) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 556 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Phe	Ser	Phe	Gly	Gly	Asn	Ile	Glu	Lys	Asn	Lys	Gly	Ile	Phe	1	5	10	15
Lys	Leu	Trp	Ala	Pro	Tyr	Val	Asn	Ser	Val	Lys	Leu	Lys	Leu	Ser	20	25	30	35
Lys	Lys	Leu	Ile	Pro	Met	Glu	Lys	Asn	Asp	Glu	Gly	Phe	Phe	Glu	40	45	50	55
Val	Glu	Ile	Asp	Asp	Ile	Glu	Glu	Asn	Leu	Thr	Tyr	Ser	Tyr	Ile	60	65	70	75
Ile	Glu	Asp	Lys	Arg	Glu	Ile	Pro	Asp	Pro	Ala	Ser	Arg	Tyr	Gln	80	85	90	95
Pro	Leu	Gly	Val	His	Asp	Lys	Ser	Gln	Leu	Ile	Arg	Thr	Asp	Tyr	100	105	110	115
Gln	Ile	Leu	Asp	Leu	Gly	Lys	Val	Lys	Ile	Glu	Asp	Leu	Ile	Ile	120	125	130	135
Tyr	Glu	Leu	His	Val	Gly	Thr	Phe	Ser	Gln	Glu	Gly	Asn	Phe	Lys	140	145	150	155
Gly	Val	Ile	Glu	Lys	Leu	Asp	Tyr	Leu	Lys	Asp	Leu	Gly	Ile	Thr	160	165	170	175
Gly	Ile	Glu	Leu	Met	Pro	Val	Ala	Gln	Phe	Pro	Gly	Asn	Arg	Asp	180	185	190	195
Trp	Gly	Tyr	Asp	Gly	Val	Phe	Leu	Tyr	Ala	Val	Gln	Asn	Thr	Tyr	200	205	210	215
Gly	Gly	Pro	Trp	Glu	Leu	Ala	Lys	Leu	Val	Asn	Glu	Ala	His	Lys	220	225	230	235
Arg	Gly	Ile	Ala	Val	Ile	Leu	Asp	Val	Val	Tyr	Asn	His	Ile	Gly	240	245	250	255
Pro	Glu	Gly	Asn	Tyr	Leu	Leu	Gly	Leu	Gly	Pro	Tyr	Phe	Ser	Asp	260	265	270	275
Arg	Tyr	Lys	Thr	Pro	Trp	Gly	Leu	Thr	Phe	Asn	Phe	Asp	Asp	Arg	280	285	290	295
Gly	Cys	Asp	Gln	Val	Arg	Lys	Phe	Ile	Leu	Glu	Asn	Val	Glu	Tyr	300	305	310	315
Trp	Phe	Lys	Thr	Phe	Lys	Ile	Asp	Gly	Leu	Arg	Leu	Asp	Ala	Val	320	325	330	335
His	Ala	Ile	Phe	Asp	Asn	Ser	Pro	Lys	His	Ile	Leu	Gln	Glu	Ile	340	345	350	355
Ala	Glu	Lys	Ala	His	Gln	Leu	Gly	Lys	Phe	Val	Ile	Ala	Glu	Ser	360	365	370	375
Asp	Leu	Asn	Asp	Pro	Lys	Ile	Val	Lys	Asp	Asp	Cys	Gly	Tyr	Lys	380	385	390	395
Ile	Asp	Ala	Gln	Trp	Val	Asp	Asp	Phe	His	His	Ala	Val	His	Ala	400	405	410	415
Phe	Ile	Thr	Lys	Glu	Lys	Asp	Tyr	Tyr	Tyr	Gln	Asp	Phe	Gly	Arg	420	425	430	435
Ile	Glu	Asp	Ile	Glu	Lys	Thr	Phe	Lys	Asp	Val	Phe	Val	Tyr	Asp	440	445	450	455

Gly Lys Tyr Ser Arg Tyr Arg Gly Arg Thr His Gly Ala Pro Val
 350 355 360
 Gly Asp Leu Pro Pro Arg Lys Phe Val Val Phe Ile Gln Asn His
 365 370 375
 5 Asp Gln Val Gly Asn Arg Gly Asn Gly Glu Arg Leu Ser Ile Leu
 380 385 390
 Thr Asp Lys Thr Thr Tyr Leu Met Ala Ala Thr Leu Tyr Ile Leu
 395 400 405
 Ser Pro Tyr Ile Pro Leu Ile Phe Met Gly Glu Glu Tyr Tyr Glu
 10 410 415 420
 Thr Asn Pro Phe Phe Phe Ser Asp Phe Ser Asp Pro Val Leu
 425 430 435
 Ile Lys Gly Val Arg Glu Gly Arg Leu Lys Glu Asn Asn Gln Met
 440 445 450
 15 Ile Asp Pro Gln Ser Glu Glu Ala Phe Leu Lys Ser Lys Leu Ser
 455 460 465
 Trp Lys Ile Asp Glu Glu Val Leu Asp Tyr Tyr Lys Gln Leu Ile
 470 475 480
 Asn Ile Arg Lys Arg Tyr Asn Asn Cys Lys Arg Val Lys Glu Val
 485 490 495
 20 Arg Arg Glu Gly Asn Cys Ile Thr Leu Ile Met Glu Lys Ile Gly
 500 505 510
 Ile Ile Ala Ser Phe Asp Asp Ile Val Ile Asn Ser Lys Ile Thr
 515 520 525
 25 Gly Asn Leu Leu Ile Gly Ile Gly Phe Pro Lys Lys Leu Lys Lys
 530 535 540
 Asp Glu Leu Ile Lys Val Asn Arg Gly Val Gly Val Tyr Gln Leu
 545 550 555
 Glu

30

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1668 base pairs

(B) TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGTTTTCGT TCGGTGGAAA TATTGAAAAA AATAAAGGTA TCTTTAAGTT ATGGGCACCT 60
 TATGTTAATA GTGTTAAGCT GAAGTTAAGC AAAAAACTTA TTCCAATGGA AAAAAACGAT 120
 40 GAGGGATTTT TCGAAGTAGA AATAGACGAT ATCGAGGAAA ATTTAACCTA TTCTTATATT 180
 ATAGAAGATA AGAGAGAGAT ACCTGATCCC GCATCAGCAT ATCAACCTTT AGGAGTTCAT 240
 GACAAATCAC AACTTATAAG AACAGATTAT CAGATTCTTG ACCTTGGAAA AGTAAAAATA 300
 GAAGATCTAA TAATATATGA ACTCCACGTT GGTACTTTTT CCAAGAAGG AAATTTCAAA 360
 GGAGTAATAG AAAAGTTAGA TTACCTCAAG GATCTAGGAA TCACAGGAAT TGAAGTATG 420
 CCTGTGGCAC AATTTCCAGG GAATAGAGAT TGGGGATACG ATGGTGTGTTT TCTATACGCA 480
 45 GTTCAAAATA CTTATGGCGG ACCATGGGAA TTGGCTAAGC TAGTAAACGA GGCACATAAA 540
 AGGGGAATAG CCGTAATTTT GGATGTTGTA TATAATCATA TAGGTCCTGA GGGAAATTAC 600
 CTTTTAGGAT TAGGTCCTTA TTTTTCAGAC AGATATAAAA CTCCATGGGG ATTAACATTT 660
 AATTTTGATG ATAGGGGATG TGATCAAGTT AGAAAATTCA TTTTAGAAAA TGTCGAGTAT 720
 TGGTTTAAGA CCTTTAAAT CGATGGTCTG AGACTGGATG CAGTTCATGC AATTTTGTAT 780
 50 AATTCGCCTA AGCATATCCT CCAAGAGATA GCTGAAAAAG CCCATCAATT AGGAAAATTT 840
 GTTATTGCTG AAAGTGATT AAATGATCCA AAAATAGTAA AAGATGATTG TGGATATAAA 900
 ATAGATGCTC AATGGGTTGA CGATTTCCAC CACGCAGTTC ATGCATTCAT AACCAGAA 960
 AAAGATTATT ATTACCAGGA TTTTGAAGG ATAGAAGATA TAGAGAAAAC TTTTAAAGAT 1020
 GTTTTTGTTT ATGATGGAAA GTATTCTAGA TACAGAGGAA GAACTCATGG TGCTCCTGTA 1080
 55 GGTGATCTTC CACCACGTAA ATTTGTAGTC TTCATACAAA ATCAGCATCA AGTAGGAAAT 1140

AGAGGAAATG GGGAAAGACT TTCCATATTA ACCGATAAAA CGACATACCT TATGGCAGCC 1200
 ACACATATATA TACTCTCACC GTATATACCG CTAATATTTA TGGGCGAGGA ATATTATGAG 1260
 ACGAATCCTT TTTTCTTCTT CTCTGATTTC TCAGATCCCG TATTAATTAA GGGTGTTAGA 1320
 5 GAAGGTAGAC TAAAGGAAAA TAATCAAATG ATAGATCCAC AATCTGAGGA AGCGTTCTTA 1380
 AAGAGTAAAC TTTCATGGAA AATTGATGAG GAAGTTTGTAG ATTATTATAA ACAACTGATA 1440
 AATATCAGAA AGAGATATAA TAATTGTAAA AGGGTAAAGG AAGTTAGGAG AGAAGGGAAC 1500
 TGTATTACTT TGATCATGGA AAAAATAGGA ATAATTGCAT CGTTTGATGA TATTGTAATT 1560
 AATTCTAAAA TTACAGGTAA TTTACTTATA GGCATAGGAT TTCCGAAAAA ATTGAAAAAA 1620
 GATGAATTAA TTAAGGTAA CAGAGGTGTT GGGGTATATC AATTAGAA 1668

(3) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Phe	Ser	Phe	Gly	Gly	Asn	Ile	Glu	Lys	Asn	Lys	Gly	Ile	Phe
1				5					10					15
Lys	Leu	Trp	Ala	Pro	Tyr	Val	Asn	Ser	Val	Lys	Leu	Lys	Leu	Ser
				20					25					30

(4) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ile	Asp	Ala	Gln	Trp	Val	Asp	Asp	Phe	His	His	Ala	Val	His	Ala
1				5					10					15
Phe	Ile	Thr	Lys											

(5) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1668 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Sulfolobus acidocaldarius

(B) INDIVIDUAL ISOLATE: ATCC 33909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG	TTT	TCG	TTC	GGT	GGA	AAT	ATT	GAA	AAA	AAT	AAA	GGT	ATC	TTT	AAG	48
Met	Phe	Ser	Phe	Gly	Gly	Asn	Ile	Glu	Lys	Asn	Lys	Gly	Ile	Phe	Lys	

1	TTA	TGG	GCA	CCT	TAT	GTT	AAT	AGT	GTT	AAG	CTG	AAG	TTA	AGC	AAA	AAA	96
	Leu	Trp	Ala	Pro	Tyr	Val	Asn	Ser	Val	Lys	Leu	Lys	Leu	Ser	Lys	Lys	
5	CTT	ATT	CCA	ATG	GAA	AAA	AAC	GAT	GAG	GGA	TTT	TTC	GAA	GTA	GAA	ATA	144
	Leu	Ile	Pro	Met	Glu	Lys	Asn	Asp	Glu	Gly	Phe	Phe	Glu	Val	Glu	Ile	
			35				40						45				
	GAC	GAT	ATC	GAG	GAA	AAT	TTA	ACC	TAT	TCT	TAT	ATT	ATA	GAA	GAT	AAG	192
	Asp	Asp	Ile	Glu	Glu	Asn	Leu	Thr	Tyr	Ser	Tyr	Ile	Ile	Glu	Asp	Lys	
10		50					55						60				
	AGA	GAG	ATA	CCT	GAT	CCC	GCA	TCA	CGA	TAT	CAA	CCT	TTA	GGA	GTT	CAT	240
	Arg	Glu	Ile	Pro	Asp	Pro	Ala	Ser	Arg	Tyr	Gln	Pro	Leu	Gly	Val	His	
	65					70					75					80	
	GAC	AAA	TCA	CAA	CTT	ATA	AGA	ACA	GAT	TAT	CAG	ATT	CTT	GAC	CTT	GGA	288
15	Asp	Lys	Ser	Gln	Leu	Ile	Arg	Thr	Asp	Tyr	Gln	Ile	Leu	Asp	Leu	Gly	
				85						90					95		
	AAA	GTA	AAA	ATA	GAA	GAT	CTA	ATA	ATA	TAT	GAA	CTC	CAC	GTT	GGT	ACT	336
	Lys	Val	Lys	Ile	Glu	Asp	Leu	Ile	Ile	Tyr	Glu	Leu	His	Val	Gly	Thr	
				100						105							
20	TTT	TCC	CAA	GAA	GGA	AAT	TTC	AAA	GGA	GTA	ATA	GAA	AAG	TTA	GAT	TAC	384
	Phe	Ser	Gln	Glu	Gly	Asn	Phe	Lys	Gly	Val	Ile	Glu	Lys	Leu	Asp	Tyr	
			115				120						125				
	CTC	AAG	GAT	CTA	GGA	ATC	ACA	GGA	ATT	GAA	CTG	ATG	CCT	GTG	GCA	CAA	432
	Leu	Lys	Asp	Leu	Gly	Ile	Thr	Gly	Ile	Glu	Leu	Met	Pro	Val	Ala	Gln	
			130				135						140				
25	TTT	CCA	GGG	AAT	AGA	GAT	TGG	GGA	TAC	GAT	GGT	GTT	TTT	CTA	TAC	GCA	480
	Phe	Pro	Gly	Asn	Arg	Asp	Trp	Gly	Tyr	Asp	Gly	Val	Phe	Leu	Tyr	Ala	
	145					150					155					160	
	GTT	CAA	AAT	ACT	TAT	GGC	GGA	CCA	TGG	GAA	TTG	GCT	AAG	CTA	GTA	AAC	528
	Val	Gln	Asn	Thr	Tyr	Gly	Gly	Pro	Trp	Glu	Leu	Ala	Lys	Leu	Val	Asn	
				165						170						175	
30	GAG	GCA	CAT	AAA	AGG	GGA	ATA	GCC	GTA	ATT	TTG	GAT	GTT	GTA	TAT	AAT	576
	Glu	Ala	His	Lys	Arg	Gly	Ile	Ala	Val	Ile	Leu	Asp	Val	Val	Tyr	Asn	
				180						185						190	
	CAT	ATA	GGT	CCT	GAG	GGA	AAT	TAC	CTT	TTA	GGA	TTA	GGT	CCT	TAT	TTT	624
35	His	Ile	Gly	Pro	Glu	Gly	Asn	Tyr	Leu	Leu	Gly	Leu	Gly	Pro	Tyr	Phe	
			195				200						205				
	TCA	GAC	AGA	TAT	AAA	ACT	CCA	TGG	GGA	TTA	ACA	TTT	AAT	TTT	GAT	GAT	672
	Ser	Asp	Arg	Tyr	Lys	Thr	Pro	Trp	Gly	Leu	Thr	Phe	Asn	Phe	Asp	Asp	
			210				215						220				
40	AGG	GGA	TGT	GAT	CAA	GTT	AGA	AAA	TTC	ATT	TTA	GAA	AAT	GTC	GAG	TAT	720
	Arg	Gly	Cys	Asp	Gln	Val	Arg	Lys	Phe	Ile	Leu	Glu	Asn	Val	Glu	Tyr	
	225					230					235					240	
	TGG	TTT	AAG	ACC	TTT	AAA	ATC	GAT	GGT	CTG	AGA	CTG	GAT	GCA	GTT	CAT	768
	Trp	Phe	Lys	Thr	Phe	Lys	Ile	Asp	Gly	Leu	Arg	Leu	Asp	Ala	Val	His	
				245						250						255	
45	GCA	ATT	TTT	GAT	AAT	TCG	CCT	AAG	CAT	ATC	CTC	CAA	GAG	ATA	GCT	GAA	816
	Ala	Ile	Phe	Asp	Asn	Ser	Pro	Lys	His	Ile	Leu	Gln	Glu	Ile	Ala	Glu	
				260					265						270		
	AAA	GCC	CAT	CAA	TTA	GGA	AAA	TTT	GTT	ATT	GCT	GAA	AGT	GAT	TTA	AAT	864
	Lys	Ala	His	Gln	Leu	Gly	Lys	Phe	Val	Ile	Ala	Glu	Ser	Asp	Leu	Asn	
50			275				280						285				
	GAT	CCA	AAA	ATA	GTA	AAA	GAT	GAT	TGT	GGA	TAT	AAA	ATA	GAT	GCT	CAA	912
	Asp	Pro	Lys	Ile	Val	Lys	Asp	Asp	Cys	Gly	Tyr	Lys	Ile	Asp	Ala	Gln	
			290				295					300					
55	TGG	GTT	GAC	GAT	TTC	CAC	CAC	GCA	GTT	CAT	GCA	TTC	ATA	ACC	AAA	GAA	960
	Trp	Val	Asp	Asp	Phe	His	His	Ala	Val	His	Ala	Phe	Ile	Thr	Lys	Glu	

	305				310				315				320				
	AAA	GAT	TAT	TAT	TAC	CAG	GAT	TTT	GGA	AGG	ATA	GAA	GAT	ATA	GAG	AAA	1008
	Lys	Asp	Tyr	Tyr	Tyr	Gln	Asp	Phe	Gly	Arg	Ile	Glu	Asp	Ile	Glu	Lys	
					325				330						335		
5	ACT	TTT	AAA	GAT	GTT	TTT	GTT	TAT	GAT	GGA	AAG	TAT	TCT	AGA	TAC	AGA	1056
	Thr	Phe	Lys	Asp	Val	Phe	Val	Tyr	Asp	Gly	Lys	Tyr	Ser	Arg	Tyr	Arg	
				340					345						350		
	GGA	AGA	ACT	CAT	GGT	GCT	CCT	GTA	GGT	GAT	CTT	CCA	CCA	CGT	AAA	TTT	1104
10	Gly	Arg	Thr	His	Gly	Ala	Pro	Val	Gly	Asp	Leu	Pro	Pro	Arg	Lys	Phe	
			355					360						365			
	GTA	GTC	TTC	ATA	CAA	AAT	CAC	GAT	CAA	GTA	GGA	AAT	AGA	GGA	AAT	GGG	1152
	Val	Val	Phe	Ile	Gln	Asn	His	Asp	Gln	Val	Gly	Asn	Arg	Gly	Asn	Gly	
			370				375					380					
	GAA	AGA	CTT	TCC	ATA	TTA	ACC	GAT	AAA	ACG	ACA	TAC	CTT	ATG	GCA	GCC	1200
15	Glu	Arg	Leu	Ser	Ile	Leu	Thr	Asp	Lys	Thr	Thr	Tyr	Leu	Met	Ala	Ala	
	385					390				395						400	
	ACA	CTA	TAT	ATA	CTC	TCA	CCG	TAT	ATA	CCG	CTA	ATA	TTT	ATG	GGC	GAG	1248
	Thr	Leu	Tyr	Ile	Leu	Ser	Pro	Tyr	Ile	Pro	Leu	Ile	Phe	Met	Gly	Glu	
					405				410						415		
20	GAA	TAT	TAT	GAG	ACG	AAT	CCT	TTT	TTC	TTC	TTC	TCT	GAT	TTC	TCA	GAT	1296
	Glu	Tyr	Tyr	Glu	Thr	Asn	Pro	Phe	Phe	Phe	Phe	Ser	Asp	Phe	Ser	Asp	
				420				425						430			
	CCC	GTA	TTA	ATT	AAG	GGT	GTT	AGA	GAA	GGT	AGA	CTA	AAG	GAA	AAT	AAT	1344
	Pro	Val	Leu	Ile	Lys	Gly	Val	Arg	Glu	Gly	Arg	Leu	Lys	Glu	Asn	Asn	
			435				440						445				
25	CAA	ATG	ATA	GAT	CCA	CAA	TCT	GAG	GAA	GCG	TTC	TTA	AAG	AGT	AAA	CTT	1392
	Gln	Met	Ile	Asp	Pro	Gln	Ser	Glu	Glu	Ala	Phe	Leu	Lys	Ser	Lys	Leu	
	450					455						460					
	TCA	TGG	AAA	ATT	GAT	GAG	GAA	GTT	TTA	GAT	TAT	TAT	AAA	CAA	CTG	ATA	1440
	Ser	Trp	Lys	Ile	Asp	Glu	Glu	Val	Leu	Asp	Tyr	Tyr	Lys	Gln	Leu	Ile	
30	465				470				475						480		
	AAT	ATC	AGA	AAG	AGA	TAT	AAT	AAT	TGT	AAA	AGG	GTA	AAG	GAA	GTT	AGG	1488
	Asn	Ile	Arg	Lys	Arg	Tyr	Asn	Asn	Cys	Lys	Arg	Val	Lys	Glu	Val	Arg	
				485					490						495		
	AGA	GAA	GGG	AAC	TGT	ATT	ACT	TTG	ATC	ATG	GAA	AAA	ATA	GGA	ATA	ATT	1536
35	Arg	Glu	Gly	Asn	Cys	Ile	Thr	Leu	Ile	Met	Glu	Lys	Ile	Gly	Ile	Ile	
				500				505					510				
	GCA	TCG	TTT	GAT	GAT	ATT	GTA	ATT	AAT	TCT	AAA	ATT	ACA	GGT	AAT	TTA	1584
	Ala	Ser	Phe	Asp	Asp	Ile	Val	Ile	Asn	Ser	Lys	Ile	Thr	Gly	Asn	Leu	
			515				520						525				
40	CTT	ATA	GGC	ATA	GGA	TTT	CCG	AAA	AAA	TTG	AAA	AAA	GAT	GAA	TTA	ATT	1632
	Leu	Ile	Gly	Ile	Gly	Phe	Pro	Lys	Lys	Leu	Lys	Lys	Asp	Glu	Leu	Ile	
		530				535						540					
	AAG	GTT	AAC	AGA	GGT	GTT	GGG	GTA	TAT	CAA	TTA	GAA					1668
	Lys	Val	Asn	Arg	Gly	Val	Gly	Val	Tyr	Gln	Leu	Glu					
45	545				550			555									

(6) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTGCAGTTTT TTAATAAAAT CAGGAGGAAA AAAT 34

(7) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 base pairs and 4 single bases

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthesized DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

5'-TGAAGCTTGA GCT-3'

3'-ACTTCGAAC -5'

Claims

1. A recombinant thermostable enzyme having the following physicochemical properties:

(1) Action

Releasing trehalose from non-reducing saccharides having a trehalose structure as an end unit and a degree of glucose polymerization of at least 3;

(2) Molecular weight

About 54,000-64,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE);

(3) Isoelectric point (pI)

About 5.6-6.6 on isoelectrophoresis; and

(4) Thermostability

Substantially not inactivated even when incubated in an aqueous solution (pH 7.0) at 85°C for 60 min.

2. The recombinant thermostable enzyme as claimed in claim 1, which has an amino acid sequence selected from the group consisting of the amino acid sequence from the N-terminal in SEQ ID NO:1, and homologous amino acid sequences to it.

3. A DNA encoding the recombinant thermostable enzyme as claimed in claim 1.

4. The DNA as claimed in claim 3, which contains a base sequence selected from the group consisting of the base sequence from the 5'-terminus in SEQ ID NO:2, homologous base sequences to it, and complementary base sequences to these base sequences

5. The DNA as claimed in claim 3, wherein one or more bases in SEQ ID NO:2 are replaced with other bases by means of the degeneracy of genetic code without alternating the amino acid sequence in SEQ ID NO:1.

6. The DNA as claimed in claim 3, which is derived from a microorganism of the genus *Sulfolobus*.

7. A replicable DNA which contains a self-replicable vector and a DNA encoding the recombinant thermostable enzyme of claim 1.

8. The replicable recombinant DNA as claimed in claim 7, which has a base sequence selected from the group consisting of the base sequence from the 5'-terminus in SEQ ID NO:2, homologous base sequences to it, and complementary base sequences to these base sequences.

9. The replicable recombinant DNA as claimed in claim 7, wherein one or more bases in SEQ ID NO:2 are replaced with other bases by means of the degeneracy of genetic code without alternating the amino acid sequence in SEQ

ID NO:1.

10. The replicable recombinant DNA, wherein said DNA is derived from a microorganism of the genus *Sulfolobus*.

11. The replicable recombinant DNA as claimed in claim 7, wherein said self-replicabl vector is plasmid vector Bluescript II SK(+).

12. A transformant which is obtainable by introducing into an appropriate host a replicable recombinant DNA containing a self-replicable vector and a DNA encoding the recombinant thermostable enzyme of claim 1.

13. The transformant as claimed in claim 12, wherein said DNA has a base sequence selected from the group consisting of the base sequence from the 5'-terminus in SEQ ID NO:2, homologous base sequences to it, and complementary base sequences to these base sequences.

14. The transformant as claimed in claim 12, wherein said DNA is prepared by replacing one or more bases in SEQ ID NO:2 with other bases by means of the degeneracy of genetic code without alternating the amino acid sequence in SEQ ID NO:1.

15. The transformant as claimed in claim 12, wherein said DNA is derived from a microorganism of the genus *Sulfolobus*.

16. The transformant as claimed in claim 12, wherein said self-replicable vector is plasmid vector Bluescript II SK(+).

17. The transformant as claimed in claim 12, wherein said host is a microorganism of the species *Escherichia coli*.

18. A process for preparing a recombinant thermostable enzyme, which comprises culturing a transformant prepared by introducing into an appropriate host a replicable recombinant DNA containing a self-replicable vector and a DNA encoding the recombinant thermostable enzyme of claim 1, and collecting the formed recombinant thermostable enzyme from the culture.

19. The process as claimed in claim 18, wherein said DNA contains a base sequence selected from the group consisting of the base sequence from the 5'-terminus in SEQ ID NO:2, homologous base sequences to it, and complementary base sequences to these base sequences.

20. The process as claimed in claim 18, wherein said DNA is prepared by replacing one or more bases in SEQ ID NO:2 with other bases by means of the degeneracy of genetic code without alternating the amino acid sequence in SEQ ID NO:1.

21. The process as claimed in claim 18, wherein said DNA is derived from a microorganism of the genus *Sulfolobus*.

22. The process as claimed in claim 18, wherein said self-replicable vector is plasmid vector Bluescript II SK(+).

23. The process as claimed in claim 18, wherein said host is a microorganism of the species *Escherichia coli*.

24. The process as claimed in claim 18, wherein the produced recombinant thermostable enzyme is collected by one or more techniques selected from the group consisting of centrifugation, filtration, concentration, salting out, dialysis, separatory sedimentation, ion-exchange chromatography, gel filtration chromatography, hydrophobic chromatography, affinity chromatography, gel electrophoresis and isoelectrophoresis.

25. An enzymatic conversion method, which contains a step of allowing the recombinant thermostable enzyme of claim 1 to act on a non-reducing saccharide, which has a trehalose structure as an end unit and a degree of glucose polymerization of at least 3, to release trehalose.

26. The method as claimed in claim 25, which contains a step of coexisting said recombinant thermostable enzyme in an aqueous solution containing 50 w/w % or lower of said non-reducing saccharide, on a dry solid basis, and allowing said recombinant thermostable enzyme to act on said non-reducing saccharide at a temperature exceeding 55°C.

27. The method as claimed in claim 25, wherein said non-reducing saccharide is subjected to the action of a non-reducing saccharide-forming enzyme, and the formed non-reducing saccharide is subjected to the action of said recom-

binant thermostable enzyme.

28. The method as claimed in claim 25, wherein said non-reducing saccharide is a member selected from the group consisting of α -glucosyltrehalose, α -maltosyltrehalose, α -maltotriosyltrehalose, α -maltotetraosyl-trehalose, α -mal-
topentaosyltrehalose, and mixtures thereof.

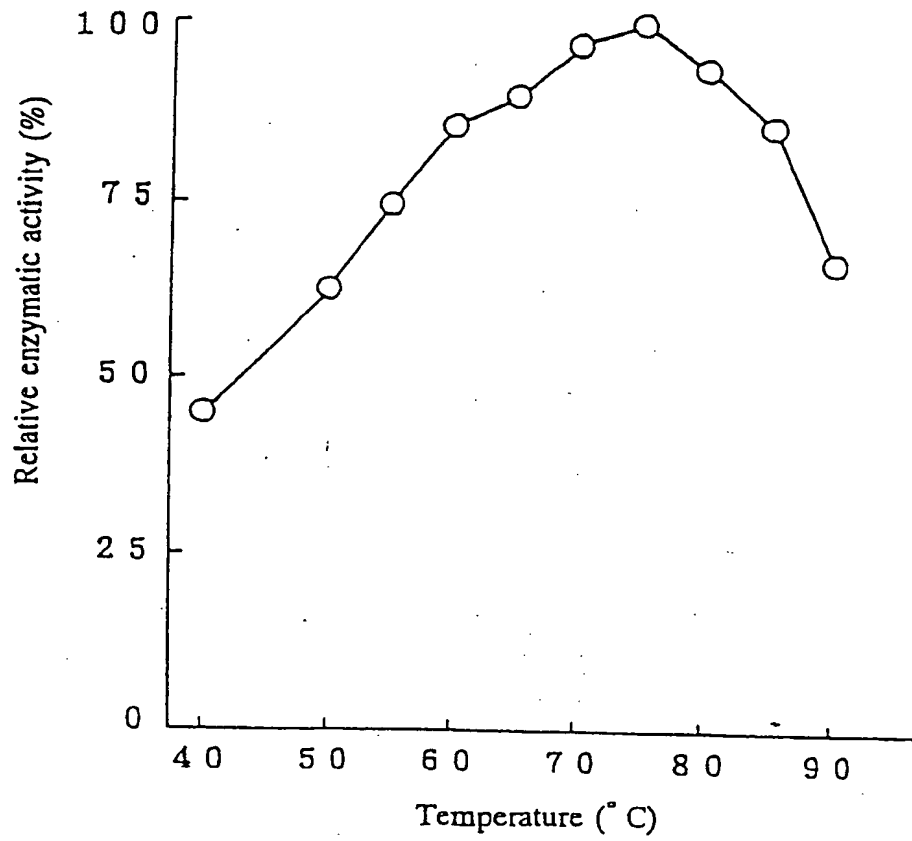


FIG.1

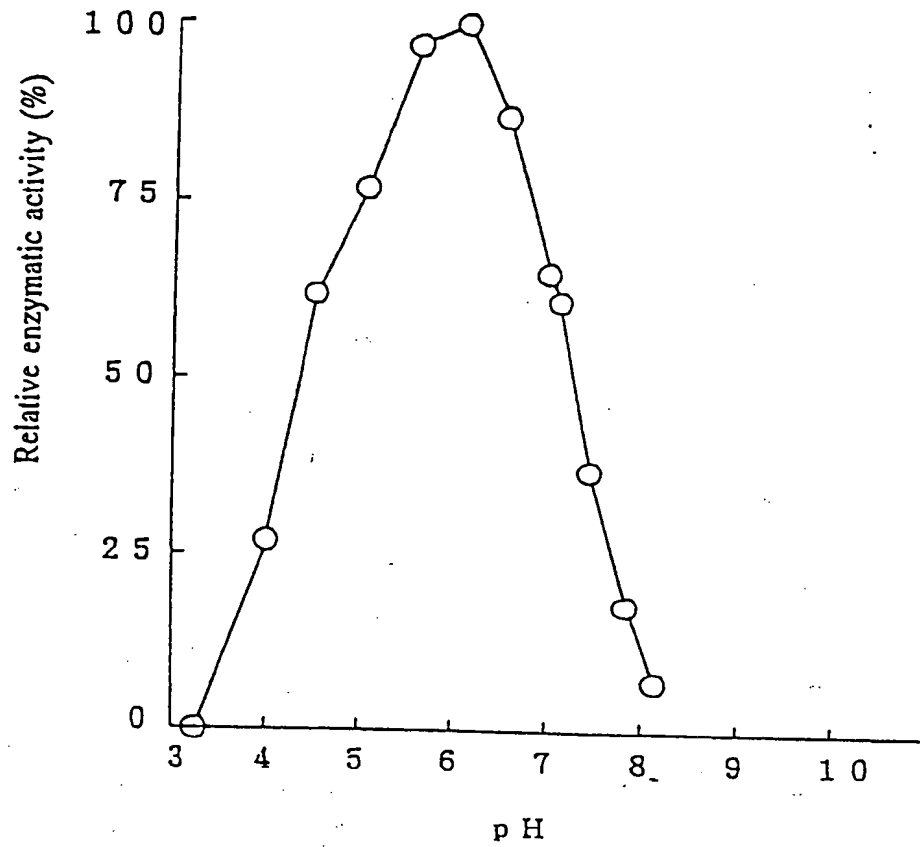


FIG.2

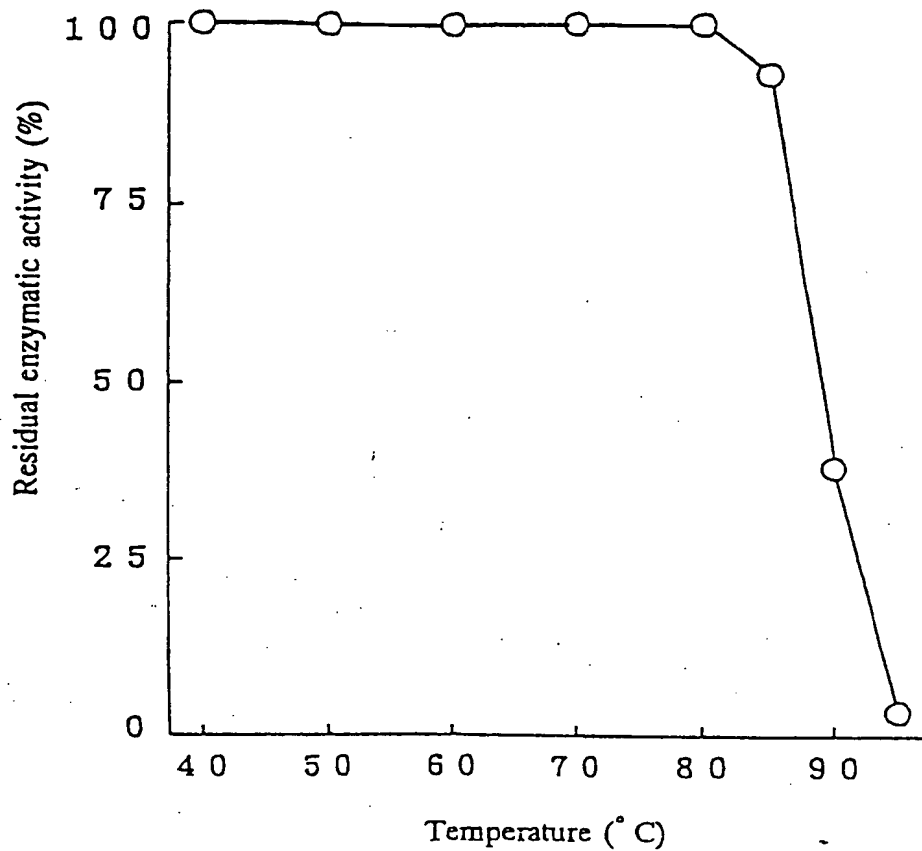


FIG.3

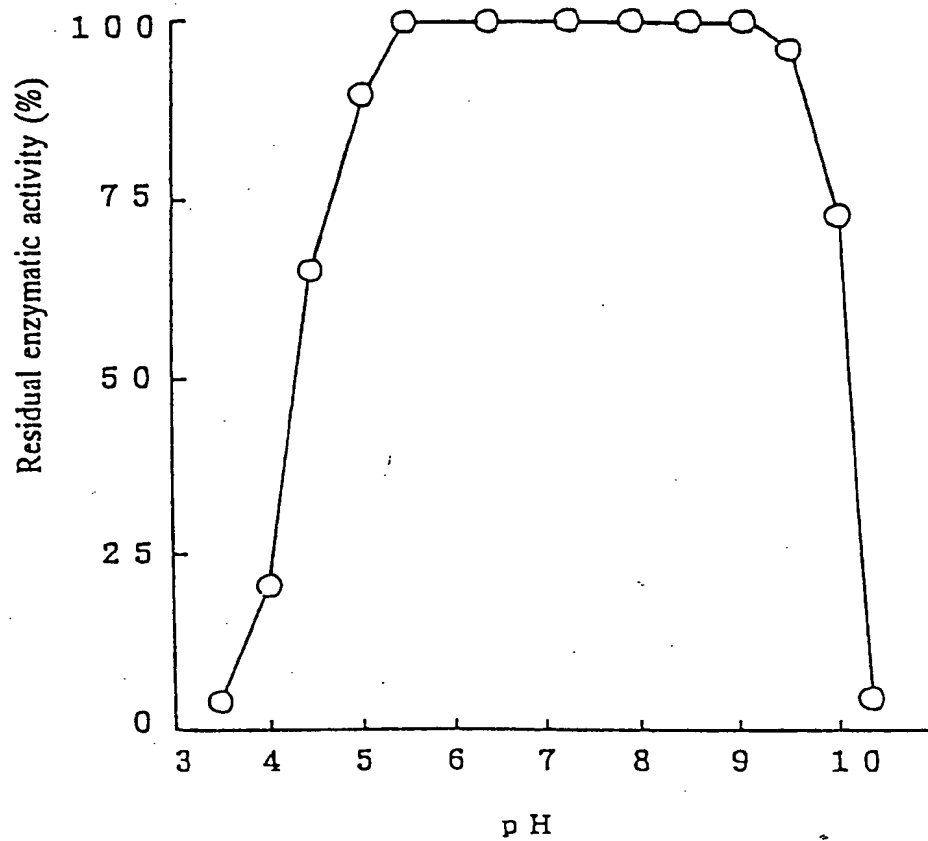


FIG.4

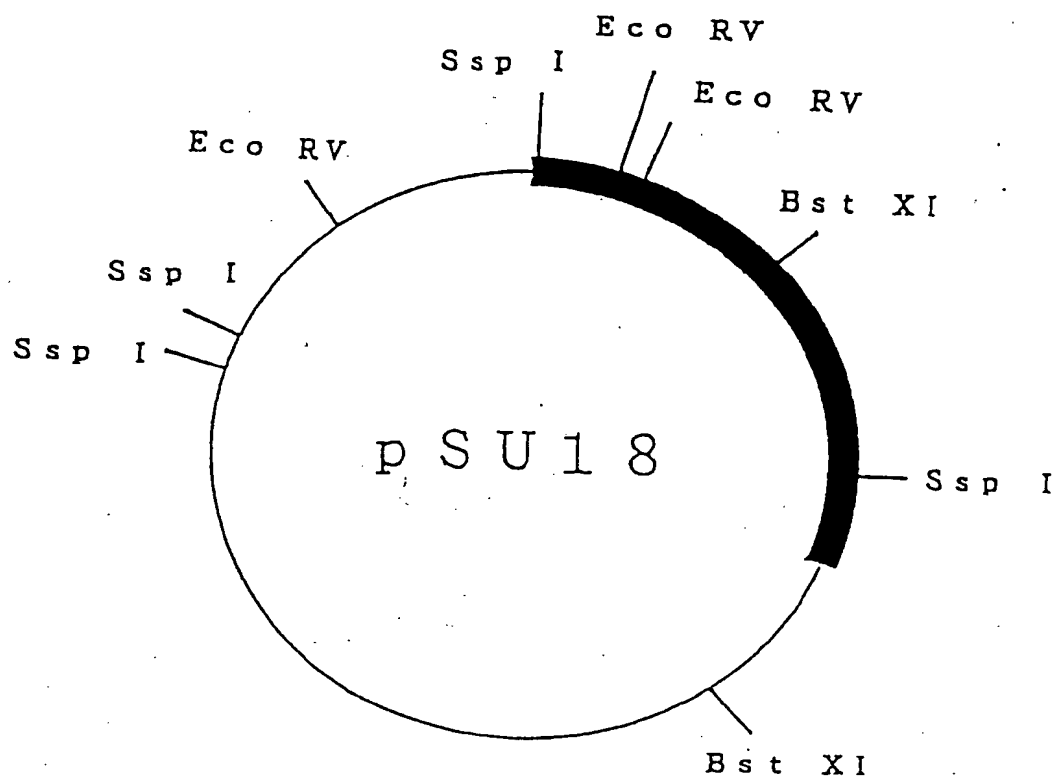


FIG.5

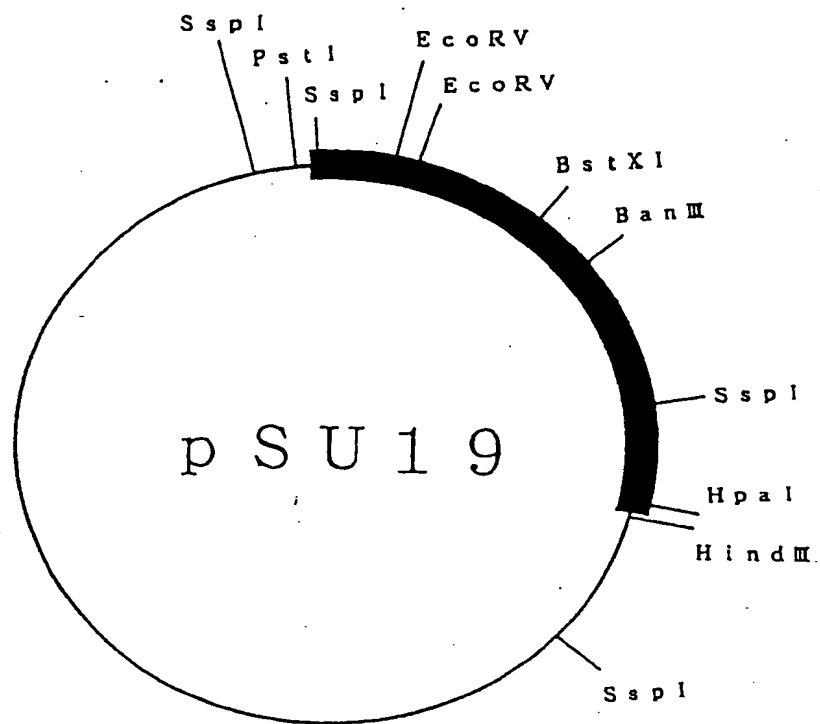


FIG.6



European Patent
Office

EUROPEAN SEARCH REPORT

Application Number
EP 95 30 5100

DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.6)
A	EP-A-0 606 753 (KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU KENKYUJO) 20 July 1994 * page 3, line 54 - page 4, line 8 * * page 8, line 54 - page 9, line 14 * * page 9, line 23 - line 43 *	1, 25-28	C12N15/56 C12N9/24 C12N1/21 C12P19/12 C12P19/14
D	& JP-A-07 143 876		
A	BIOTECH FORUM EUR. (1991), 8(4), 201-3 CODEN: BFOEEW; ISSN: 0938-7501, 1991 LAMA, LICIA ET AL 'Thermostable amylolytic activity from Sulfolobus solfataricus' * page 201, left column, paragraph 4 - right column, paragraph 1 * * page 202, middle column, paragraph 2 - page 203, left column, paragraph 3 * * page 203, left column, last paragraph - middle column, paragraph 2 *	1, 25-28	
			TECHNICAL FIELDS SEARCHED (Int.Cl.6)
			C12N C12P
The present search report has been drawn up for all claims			
Place of search THE HAGUE		Date of completion of the search 24 October 1995	Examiner Montero Lopez, B
<p>CATEGORY OF CITED DOCUMENTS</p> <p>X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document</p> <p>T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document</p>			

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